

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCGGAGCAGCACGGCGCAGGACCTGGAGCTCCGGCTGCGTCTCCCG
CAGCGCTACCCGCCATCGCCTGCGCGCCGGCGCTGGGCTCTGCCGCTTGCTG
CTGCTGCCGCCGCGAGGCGCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGCT
GGTGGACAAGTTAACAGGGGATGGTGACACCGCAAAGAAGAACCTTGGCGGGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTAGCAGTCAGCAGATTGCCCTGAGATC
CTGGAGGGCTGTGCGAGAGCAGCGACTTCAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCTGGTGGCTGCAGCTGAAGAGCGAATTCCTGACTTATTGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGGCCACTGCAGCGGAGATGGAGCAGACA
GGGCGACGGTCTCGGGTGCACATGGGTACCAAGGGCCGCTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGAAGACGTGCTCGGGCTGACCAACAGAGACTGCGGGAGTGTGAAGTGGCTGGTGT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCAGCCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACCGCTCTACACGTGCGGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTCTGGCTACCGAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGAGTGTCACTAGCAGAAAAACCTGTGTGAGGAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGCTGTGTGTGCTGCAGGGCTTCGAAGAAAACG
GAAGATGCTGTGTGCGCCGGCAGAGGCTGAAGGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGGAAGACCTGAATGTGCCGGAACCTACCCCTTAAATTATTCAAGGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCCTGCACTGGACAGCGGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGCCCCAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATTTGATACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAAGCAG
TTGGCGCCATGGCCAACCTGTTATTGAGCTTACGCTTAAATGGTTACAAATAAGCAATAGCA
TCACAATTTCACAATAAACGATTTCGACTGCAATTCTAGTTGTGGTTGTTCTGAAAT
ATCAATGTTATCTTACATGTCGGATCGGGAAATTAACTGGCGCAGCACCATGGCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGGGGAAAGAACAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGAAAGTCCCAGGCTCCCAGCAGGCCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, PI: 4.53, NX(S/T): 2

MRLPRAALGLPLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDPECNQMLEAQEEHLAEAWLQLKSEYPDLFEWFCVKTALKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPCTDCMDGYFSSLRNEHTSICTADESCKTCGILTNRDCGECEVGWVLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAGTCACCTCGGTTATCGATTGAATTCCCGGGATCCCTAGAGATCCCTC
GACCTCGACCCACCGCGTCGCCAGGCCAGGCGACGCCAGCTAAACGGAAACA
GCCCTGGCTAGGGAGCTGCAGCGCAGCAGAGTATCTGACGCCAGGTTGGTAGGCG
GCACGAGGAGTTTCCCGCAGCAGGAGGAGGCTCTGAGCAGC**ATGGCCCGAGGAGCGCC**
CTCTGGCCCGCAGGAGGAGCCTGTAACCTATGGATGCTCTGCTGCCACTCGGGCGGAGGC
CGGGCCCGCAGGAGGAGCCTGTAACCTATGGATGCTCTGCTGCCACTCGGGCGGAGGC
TAGGATTGAAGAAGATATCTGATTGTTAGGGGGAAAATGGCACCTTTACACATGAT
TCAGAAAAGCGAACAGAGAACATGCGAGCTATTCTGTAATATCCATTGATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGAGAACATCTATGAAATTCTGCTTGCCTTGCCTCCGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGCTCCCTGCTGGGACAGTGCCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCCATGCTTGAAAACAGGATGGGTGGCAGCATTTGAAGT
GGATGTTGATTGTTATGAAATTCTGAGGCAACACCCATCTCCAAACACCTCAAATGCTATCT
TCCTAAAACATGTCACAAAGCTGAGTGCCTCAGGCCAGGGCTGCCAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCCACGGACCTACTGTGAGAAAGCCCTTG
TACCCACGATGATGAGTGTGAACTGGGAGCTTGTGTGACTCTGGTTCTGCATCTGCCAACCTG
GATTCTATGGAGTGAACATGTCACAAAGAACATGCTCAACCCACTGCTTAAATGGAGGAGC
TGTTCTACCCCTGAAAATGATTTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAATCAG
CAAATGCCACACCCATGCGAAATGGAGGTAATGCACTGGTAAAGCAAATGTAAGTGT
CCAAAGGTTACAGGGAGACCTCTGCAAAAGCCTGTCGAGCCTGCTGGTGCACAT
GGAAACCTGCCATGAACCCAAACATGCAATGTCAGAAGGTTGGCATGAAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC
ACACGGCTTCACTTAAAAGGCCAGGAGGCCGGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAAGTACACCAAGTCTAGCCTTGTAAACCTTCA
TGTTGTTGAATGTTCAAATAATGTTCACTACACTTAAAGAATACTGCCCTGAATTGTTATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTCTCTTAAAGTTTCTAAGTACGTCGTAG
CATGATGGTATAGATTCTGTTCTGCTTGGGACAGATTTTATATTATGTCATTGAA
TCAGGTTAAAATTCTCAGTGTGTTAGTGGCAGATATTCAAAATTACAATGCAATTATGTT
GTCTGGGGCAGGGACATCAGAAAGGTTAAATTGGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGCATTGAGATTATTGTCAGATATTAGCT
GTTTGTATCATTTTAAAATTGCTCTTAATTTTAAACTCTAACATACAATATATTGACC
TTACCAATTCTCAGAGATTCACTGATTAAAAAAATTACACTGTGTTAGTGGCATT
AAAACATATAATATATTCTAACACAACTGAAATAGGGAAATATAATGTTAGTGAACCTTTGCT
TGCTTGAAGCAATATAATATTGTAACAAAACAGCTTACCTAACATAAAACATTGAT
ACTGTTGTATGTTAAAGGTGCTGCTTGTAGTTTGAAAGAAAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTGGC
CGCCATGGCCAACTTGTATTGCGCTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLALRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNNGFCNERRICECPDPGFHGPCHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICCPPGLEGEQCEISKCPQPCRNGGKICIGKSCKCSCSKGYQGDLCSPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLLCCRGRADDC
ALPYLGAICYCSDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCTTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTCTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCCTGTCCTTNGCCCAGAACCTGCTGTCTTGTAACACCCAC
CAGCAGCAGGGCTGCCCGCAGTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCGCCAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCGTGAACGAGACGAGGCTGCCCTGCGC
CCCCCTGTATGATGCACAGGCCATGGTCGGGCAAGGCCAGGGCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCTGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCAGGTGAGCAACGAGGACTGCCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCCTGGACCGCGCGCATCCGCGCAGTTGGCCTCTGACCGTCATCAGCAAAGGCTG
CAGCTGAACTGCGTGG**ATG**ACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCTGCTGCTCTGGGGACCCGGCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCCAGGCCCTGTGCCACTCCTCACAGACCTG
GCCAGTGAGGAGCCTGTCCTGGTCAACGCCATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCTGACCCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTAACCTGTGCTCAGGCACCTTCTCCCCCAGGAAGCCTT
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCACT**AA**AGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGTTGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRRLPPSLRCSLHSACCSGDASYRLWGAPLQPT
LGVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTFPVPHPDPPMALSRTPTRQISSDT
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACACGGTCCGAACCTCTCAGCGATGGGAGCCGCCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGGCCAGGGACGGCAACAAGTTGCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGGTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGGCCAGCGGGAAAGAGCAAAGACTG
CGTGGTACGGAGATCGTGGAGAACACTATACGCCCTTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTCACGGGCAGGGGGGCCCGCCAGGCTTCCCGCAGCGCCAGAAC
CAGCGCGAGGCCACTTCATCAAGCGCCTTACCAAGGCCAGCTGCCCTCCCAACCGC
CGAGAACAGAACAGCTTCGAGTTGTGGCTCGCCCCACCCGCCGACCAAGCGCACAC
GGCGGCCAGCCCTCACGTACTCTGGAGGCAGGGGCCAGCAGCCCTGGGCCCTCC
CCCCCTTCCCTCTTAATCCAAGGACTGGCTGGGTGGCGGAGGGAGCCAGATCCCC
GGGGAGGACCTGAGGGCCCGAAGCATCCGAGCCCCCAGCTGGAAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTTCCCGACGGGTGGCAGGCCCTGGAGAGGA
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCGGGCTCTGAAGCC
CGCTGAAAGGTCAAGCGACTGAAGGCCCTTGAGACAAACCGCTGGAGGTGGCTCTCAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGAAACCTCTCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTTCAAGAAAAAAAGGGAGAGAGGAAATAG
AGGGTTGTCACCTCACATTCCACGCCAGGGCCTGCACCCACCCCAACTCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTIEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTCGACATGGAG
GACAGCAGAAAGGGCAACACAGGCTGATAAGACAGACAGCAGGGAGATTATTAC
CATACGCCCTCAGGACGTTCCCTAGCTGGAGTTCTGGAACAGAACCCCATCCAGT
CATTTGATTTGCTGTTATTCTTTCTTTCTTTCCACACATTGATTTAT
TTCGGTACTTCAGAAATGGCCTACAGACCAAAAGTGGGCCAGCCATGGGCTTTTCCT
GAAGTCTTGGCTATCATTCCCTGGGGCTACTCACAGGTGTCACAGGTTCAAACTCTGGCTG
CTAGTGTGCGCCTGCGACAGGAACCTGTACTGTAAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCGGAGGGCTAACGGTACTCTCCACAAACAAACAAATTAAATATGC
TGGATTTCCTGAGAACACTGCACAAATGTACAGCTGGTGCACAGGTCTACCTGTATGGCAAC
AACTGGACGAACTCCCCATGAACTTCCCAAGAAATGTCAAGAGTTCTCCATTGAGAAAAC
AAATTCAAGACCATTCACGGCTGCTTGGCCAGCTCTTGAAAGGCTGACCT
GGATGACAACCTCCATACCAAGTGGGGGGTGAAGGGCCCTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTGCTAAAGAACCTCAGACTGTGCTGTTGGCTTCTGTGAC
TTGCAAGAGCTGAGAGTGGATGAAATCGAATTGCTGTATACCGACATGGCTTCCAGAA
TCTCACGAGCTGGAGCTTATTGAGCAGGGAACCTCTGACCCAACAGGGTATGCCG
AGGGCACCTTCAGGACATCTCACCAAGCTCAAGAAATTTCAAATTGTACCTAATTGCTGCC
CACCCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTTATTGAGGACAACAGAT
AAACACACATTCTTGACAGCCTCTCAAATCTGCTAAAGCTGGAACGGCTGGATATACCA
ACAACCAACTGGGATGCTGACTCAAGGGGTTTGTATAATCTCTCCAAACCTGAAGCCTC
ACTGCTGGAAATAACCCCTGGGTTGTGACTCAGTAAATGGGTACAGAAATGGCTCAA
ATATATCCCTCATCTCACCGTGGGGTTCTGTGCAAGGCTCTGACAAAGTCCGGG
GGATGGCCGTCAAGGAAATTAAATGATCTTTGCTGCTGCTTCCACACGGACCCCCGGCTG
CCTCTTCACCCCAGCCCCAAGTACAGCTTCTGGCAGGACACTCAGCCTCCACCCCTCTAT
TCCAAACCTCTAGCAGAAAGCTACACGCCCTCAAACCTCTACACATCGAAACTTCCCACGATT
CTGACTGGGATGGCAGAGAAGAGTGAACCCACCTATTCTGTAACGGATCCAGCTCTTCTATC
CATTTGTGAATGATACTCCATTCAAGTCAGCTGGCTCTCTTACCGTGTGGCATA
CAAACTCACATGGGTGAAATGGGCCACAGTTAGTAGGGGCATCGTTCAGGAGCGTAG
TCAGCGGTGAGAAGCAACACTGAGCTGGTTACTTAGAGCCCCGATCCACCTATCGGATT
TGTGTTAGTGGCACTGGATGCTTTAACTACCGCGCGTGAAGAGACACCAATTGTTCAAGGGC
CACCAACCCATGCCCTCATGAAACACGGCAGAACACAGCAGCTCCAGGATGAGCAGACGA
CGTCCCACAGCATGGGCTCCCTTCTGCTGGGGCTTGATCGGGGGCGGGTGTATATT
GTGCTGGTGGCTTGTGCTAGCGTCTTTGCTGGCATATGCAAAAAGGGGGCTACACCTC
CCAGAAAGTGGAAATACAACCGGGGGCGCGAAAGATGATTATTGGAGGGCAGGACCAAGA
AGGACAACCTCATCCCTGGAGATGACAGAAACCGATTTCAAGATGCTCTTAAATAACGAT
CAACTCTAAAGGAGATTTCAGACTGCAAGCCATTACACCCAAATGGGGCATTAAATTA
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACACGAGCGTGCCAGACCTGGAGC
ACTGCCCCATACGTGACAGCCAGAGGCCAGCGTTACAGGGCAGAACATTAGACTCTTGAGAA
CACACTCGTGTGTCACATAAGACACGCGAGATTACATTGATAATGGGATTTAAAAAGTG
TTGTCATTGAAATCTGTAATTACCGGTGACTATATAATGGGATTTAAAAAGTG
CTATCTTCTATTCAAGTAAATTACAAACAGTTGTAACTCTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPMSGAFFLKSWLIIISLGLYSQVSCKLACPSVCRCDRNPVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAEHLNVQSVHTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQQLKLEELHLDNNISTVGVEDGAFREAISSLKLLFLSKNHLSSPVVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLITNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHPIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSICKWVTEWLKYIPLSSLNVRGFMCGQPEQVRGMARELNMNLLSCPTTTPGLPLFTP
APSTASPTTQPPPTLSIPNPSSRSYTPPTPTSKLPTIPDWDGRERVTPPISERIQLSIHVN
TSIQVSWLSSLFTVMAKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVP
DAFNRYRAVEDTICSEATTHASLYNNGSNTASHEQTTSHSMGSPFLLAGLIGGAVIFVLV
LSVFCWHMHKKGRYTSQWKYNRGRKDDYCEAGTKKDMSILEMTETSFQIVSLNNNDQLLG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRRHARTHQPQTLLESSCENKRADLVII
DSSRSVNTHDYAKVEFIVDILQFLDIGPDVTRVGLLQVGSTVKNEFSLKTFKRKSEVERAV
KMRMRHLSTGTMGLAIQYALNIAFSEAEAGRPLRENVPVRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIQGVQVFNTLKSISGSEPHEDHVFVLVANFSQIETLTSVQFQKKLCTAHMCSTLEHN
CAHFCINI PGSYVCRCKQGYIILNSDQTTCRQDLCAMEDHNCQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDVYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKCTRINYCALNPKGC
EHECVNMEESYYCRCHRGYTLDPNGKTCRSVHDCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPGHVRLRSRGDKTAKLDSCALGDHGCE
HSCVSSEDSFVCQCFCFGYIILEDGKTCRRKDVQCQAHGCEHICVNSDDSYTCLEGFRILA
EDGKRCRRKDVKSTHHGCEHICVNNGNSYICKCSEGFGVLAEDGRRCKCTEGPIDL VFVID
GSKSLGEENFEVVVKQFVTGIIIDLSPKAARVGLLQYSTQVHETFTLRNFNSAKDMKKAVA
HMKYMKGKGSMTGLALKHMFERSFTQEGARPLSTRVPRAAIVFTDGRAQDDVSEWASAKAN
GITMYAVGVGKAIIEEEQEIASEPTNKHLYFAEDFSTMDEISEKLKKGICEALEDSGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGCTCGCTCCCGCGCACGCTCCGGCGTCGCGCACGCTCG
GCACCTCGAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCGCCAGGGAGGGC
CATGATTTCCCTCCGGGGCCCTGGTACCCAACTTGTGCGGTTTTGTTCTGGGCTGA
GTGCCCTCGGCCCGCCCTCGGGGCCAGCTGCAACTGCACTGCCGCAACCGGTTGCAAG
GCGGTGGAGGGAGGGAAAGTGGTCTTCAGCGTGGTACACCTTGACGGGAGGTGTC
ATCCCAGCCATGGGAGGTGCCCTTGTATGTGGTTCTCAAACAGAAAAGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTCGGGCTGGAGGGTCTCCAGGAGAAAGACTCTGCCCTA
CAGCTGTCCTGTGAATGTGCAAGACAAACAAGGAAATCTAGGGCCACAGCATCAAACCT
TAGAACTCAATGTACTGGTCTCCAGCTCCTCCATCTGGCGTCTCCAGGGTGTGCCCAT
GTGGGGCAACGTGACCTGAGCTGCCAGTCTCAAGGAGTAAGCCGCTGTCAATACCA
GTGGGATCGCAGCTTCCATCTTCCAGACTTTCACAGCATTAGATGTCATCGTG
GGTCTTAAAGCCTCACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCGAAAGGCCAC
AATGAGGTGGCACTGCCAACATGTAATGTGACGCTGGAAAGTGGAGCACAGGGCTGGAGCTG
AGTGGTTGCTGGAGCTGTGTTGGTACCTGGTGGACTGGGGTGTGCTGGCTGGCTGGTGC
TCTTGTACCAACGCCGGGCAAGGCCCTGGAGGAGCCAGCAATGATATCAAGGAGGATGCC
ATTGCTCCCGGACCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC
TTCCTCTGTACCTCGCACGCCCTGGGCCACCCATGGCCCTCCAGGCCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGGCCCTGGGCCACCCATGGCCCTCCAGGCCCTGGTGC
GGGGCCACCCCAACCAATATCCCCATCCCTGGTGGGTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCTGTGATGGTCCCTGGCAAGGTCAAGCTGGCTCTGGTAT**GATGAC**
CCCCACCACTATTGGCTAAAGGATTGGGTCTCTCCTTCTATAAGGGTACCTCTAGCAC
AGAGGCTGAGTCATGGGAAAGAGTCACACTCCGTACCCCTTAAGTCTGCCCCCACCTCTC
TTTACTCTGGGAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAAGAGGA
AGTGGATCTGGAAATTGGGAGGAGCCTCCACCCACCCCTGACTCTCTTATGAAGGAGCTG
CTGAAATTAGCTACTCACCAGAGTGAGGGCAGAGACTTCCAGTCAGTGTCTCCAGGC
CCCCCTGATCTGTACCCACCCATCTAACACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTGAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGGAACTC
TTATTAACATGAAATATGTGTTGTTTCTATTGCAAATTAAATAAGGATACATAA
TGTGTTGATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTACQCNVLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAAPRTLWPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
MGAAPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCA**ATGAAACGCCTCCCGCTCCTAGTGGTTTTCCACTTG**
TTGAATTGTCCTATACTCAAATTGCAACAGACACTGTCTCCAAATGCAAATGTGA
AATACGCAATGGAATTGAAAGCTGCTATTGCAACATGGGATTTAGGAAATGGTGCACAA
TTTGTGAAGAGTATACTGAATGTGAAATTAACTCAAGTCTGTGCGAAAATGCTAATTG
ACTAACACAGAAGGAAGTTATTGTATGCTGCAAAATTAAACCTTAAACAAAATCAGATCCAG
AGACAGGTTTACTAATGATGGAACCGCTGTATAGAAAATGTGAATGCAAACCTGCCATT
TAGATAATGTCGTATAGCTGCAAAATTAAACCTTAAACAAAATCAGATCCAG
GAACCTGTGGCTTGTCTACAAGAAGTCTATAAGAAAATCTGTGACAGATCTTCACCAAACAGA
TATAATTACATATAGAAAATTAGCTGAATCATCTTCAATTACTAGGTTACAAGAACACA
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTGAATTGAAAAACCGTGAAT
AATTGGTCAACAGGATACTTGTAGTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTCAGAACATCTGCAACTGTGACAAGCTTTAAGGATATCCCAGAGCTTCC
AAAAGACCCACAGAGTTGTACAAATTCAACGGATACTGCTCAAAGTTCTTTTGTAT
TCATATAACATGAAACATATTCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGATGATTCAATGGCAATGTGCACTTGTGATTGGTATTTTATATA
AGAGTATTGGCTCTTGTCTTCACTATGCAACACTTCTATTGAAAACCTCAAATTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTCAGTAATTCTCAGTCTCAATGAGCTAACCC
ACCCACATTATGAACTTGAAGAAAATAACATTACATTAAAGTCATGAAAGGTCACAGATA
GGTATAGGAGTCTATGTCATTGGAAATTACTCACCTGTGATACCTGAAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAATGGACAGGACACCCACCTCATGCCGTGTAATCCT
GACACATTGCAATTGATGTCCTCTGGCTCTCCATTGGTATTAAAGATTATAATATTC
TAAACAGGATCACTCAACTGAAGAAATTATTCAGTGTGTTGGCATATTGCTTTT
ACCTCTGGTCTTCTCAGTGAATTCAACAGCACCAGGACAACATTCAACAAATCTTGTG
TAGCCTATTCTTGCTGAATTGTTTCTGTGTTGGATCAATACAAATACTAATAAGCTCT
TCGTGTCATATTGGCGGACTGCTACACTACTCTTTAGCTGCTTTGATGGATGTGC
ATTGAAGGCATACATCTCATCTGTCATTGGTGGTGTCACTACAAACAAAGGATTGGCA
CAAGAATTTTTATCTTGTGCTATCAAGGCCAGCGTGTGAGTTGGATTTCGGCAGCAC
TAGGATACAGATTATGGCAACACCAAGTATGTTGGCTTAGCACCAGAAAACAATT
TGGAGTTTATAGGACAGCATGCTTAATCATTCTGTATCTCTGGCTTTGGAGTCAT
CATATACAAAGTTCTGCTCACACTGCAAGGTTGAACACCAAGATTGTTGCTTGGAGACA
TAAGGCTTGTCGAAGAGGAGCCCTCGCTCTCTGTGTCCTCTGGCACCACCTGGATCTT
GGGGTTCTCCATTGGTGTGCAAGCCTACAGTGTGTTACAGCTACCTCTTCACAGTCAGCAATGC
TTCCAGGGATGTTCTATTCTCTGTGTTTATCTAGAAAAGATTCAAGAAGAAT
ATTACAGATTGTCAAAATGCCCCCTGTGTTGGATGTTAAGGTAAACATAGAGAAATG
GTGATAATTCAACACTGCACAAAATAAAATTCAAGCTGTGGATGACCAATGTATAAAA
TGACTCTCAAAATTCTCAATTATAACTAGACAAAAGTATTAAATCAGTTTCT
GTTTGTCTATAGGAACTGTAGATAAAAGTAAATTGTATCATATAGATAACTATGT
TTTCTATGTGAAATAGTCTGCAAAATAGTATTGAGATATTGGAAAGTAATTGTTT
CTCAGGAGTATCACTGCACCCAAGGAAAGATTCTTCTAACACGAGAAGTATGAA
TGTCTGAAGGAACCAACTGGCTGTGATATTCTGTGACTCGTGTGCTTGGAAACTAGTCC
CCTACCACTCGTAATGAGCTCCTATTCAAGGAACTGCAACATAAGAGAAATGAAAGGGCAGA
ATATCAACACAGTAAAAGGGATGATAAGATGTATTGAAATGAAACTGTGTTTCTGTAGAC
TAGCTGAGAAAATTGTTGACATAAAATGAAAGGAAACATTACCTTACCAATTGTT
TTGTTCTGCACTTAAATGTCACCTAAACATTAGACTCTGTGCTAAATCTGTTCTT
TTTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTCI CEDDNEC
GNLTQSCGENANCNTTEGSYYCMCVPGFRSSNQDRFITNDGTCIENVNANCHLDNV CIAA
NINKTLTKIRSIKEPVALLQEVRNSVTDLSP TDIIITYIEILAESSL LGYKNNTISAKDTL
SNSTLTFVKTVMNFVQRDTFVWDKL SVNHRRTHLTKLMHTVEQATLRIQSFSQKTT EFDT
NSTDIALKVFFFDSYNMKHIIHPHMNNMDG DYINIFPKRKAA YDSNGNVAVAFLYYYKSIGPLLS
SSDNFLLKPKQNYDNSEEEERVISSVSMSSNPFTLYELEKITFTLSHRKVTDRYRSLCAF
WNYSPDTMNGWSSEGCELTYSNETHTSCR CNHLTHFAILMSSG GPSIGKDYNILTRITQLG
IIISLICLAI CIFTFWFFSEI QSTRTTIHKNLCCSLFLAELVFLVGINTTNKLFCSIIAGL
LHYFFLAFAFWMCIEG IHLYLIVGVVIYNKGFLHKNFYIFG YLSPAVVVGFSAA LGYRYYGT
TKVCWLSTENNF IWSFIGPACLI ILVNLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGV LHV VHSAV VTAYLFTV SNAFQGMFIFLFLCVLSRKI QEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCACTAATTCAGTCAGTCATGAGCTCAAACCCACCCAC
ATTATATGAACCTGAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTACCTTC
TGGTTCTTCAGTGAATTCAAAGCACCAGGA

FIGURE 21

GCCTCCAGCCAAGAACCTGGGGCCGCTGGCGGGTGGGGAGGAGTCCCCGAAACCCGGCG
CTAAGCGAGGCCTCTCTCCCTCCCGCAGATCCGAAACGGCTGGCGGGCTACCCCGCTGGGA
CAAGAACGCCGCGCTGCCTGCCGGGGCCGGGGAGGGGCTGGGCTGGGGCGAGGCGG
GGTGTGAGTGGGTGTGCGGGGGGGAGGCTTGTATGCAATCCCGATAAGAAATGCTCGGG
TGCTTGGGCACCTACCCGTGGGGGGCGTAAAGGCGTACTATATAAGGCTGCGGGCCGGAG
CCGCGCGCCCGTCAAGCAGGAGCGCTCGCTCAGGATCTAGGGCCACGACCATCCAAACCC
GGCACTCACAGCCCCGAGCGCATCCCGTGCCTGCCCGACCTCCGCACCCCCATGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGGGGTGTGGTGGTACAGTATGG
ATCCTGGCGGGCCTCTGGCTGGCGGCCCTCGCCTTCGGACGGCGGGCC
CCACGTGCACTACGGCTGGGGGACCCCCATCGCCGTCGGCACCTGTACACCTCGGGGGCC
ACGGGCTCTCAGCTGCTTCTGCGCATCCGTGCCGACCCGCTGTGACTGCGCGGGGC
CAGAGCGCGCACAGTGTGGAGGATCAAGGCGACTCGCTCGGGACCCGTGGCCATCAAGG
CGTGCACAGCGTGGCTACCTCTGCATGGGCCCGAGCGCAAGATGAGGGCTGCTCAGT
ACTCGGAGGAAGACTGTGTTCTGAGGAGGAGATCGCCCGAGATGGCTACAATGTGACCGA
TCCGGAGAACGCTCCCGTCCCTCGAGCAGTGGCAAAACAGGGCAGCTGTAACAGAA
CAGAGGCTTTCTTCAACTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGGCTG
AGAACCTCAGGGGCACTTGGAAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTCAACCGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTAACT
GAGACCATGCCGGGCTTCTACTGCTGTCAGGCTGGTACCTGCGAGCGTGGGGAGC
TGCTTCTACAAGAACAGTCTCTGAGTCCACCTCTGTGTTAGCTTCTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTTCAATTGGCAGTGCAGTTCTAGCCAATAGACTTGTCTGAT
CATAAACATTGTAAGCGTAGCTTGGCCCACTGCTGCCCTGGGCCCCATTCTGCTCCCTCGA
GGTGTGTCAGGACAAAGCTGCTGCACTGTCAGTCTGCTGTTGAATACCTCCTCATCGATGGGAAC
TCACITCTTTGGAAAAAATTCTTATGTCAGGCTGAATTCTCTAATTCTCATCACTTC
CCCAAGGAGCAGCCAGAAGACAGGCACTGTTTAATTCAAGGAACAGGTGATCCACTCTGA
AAACAGCAGGTAATTTCACTCAACCCCATGTTGGGAATTGATCTATATCTACTTCCAGG
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGACTGACTGGAGCAGGCATGCCAACAG
GCTTCAGGAGTAGGGGAAGGCCGCTGGAGGCCCACTCCAGCCCTGGGACAACCTTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTCTGAGAATAACTTGCTGTCCGGTGTCACTCTGC
TTCCCATCTCCCAAGCCCCAACAGCCCTCTGCCACCTCATGCCCTCCCATGGATTGGGGCCT
CCCAAGGCCCCCACCTTATGTCACCTGCACTTCTGTCAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCCAAGTCTGTCAATAACTTGTGCTGTGAGAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCCAGCAGTGGTTTCAACATGATATACTTGTAGTAATTATTTGATATGTACA
TCTCTTATTTCTTACATTATTATGCCCCAAATTATATTATTTGATGTAGTGAAGTGGAGTTG
TTTGATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEET
EIRPDGYNVYRSEKHLPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPPLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCAGAAGTCAAGGGCCCCGGCTCCTGCGCTCTGCCGCCGGACCTCGACCTCCTCA
GAGCAGCGGCTGCCGGGGAAAGATGGCAGGAGGAGGCCGCCCTCCTCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAAGGCATGGGTTCTGCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA
AGAAGACTGTTCCCTCCAGATTAGAGTGGAAAGAACTGGTGGACTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAAGATTTCAATATCCG
GATCAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACAGTCAGTCAGTATTAGTGGCTCAGCAGTT
CCATCATGTGAAGTACCCCTCTCTGCTGTGGAACTGTGGTAGAGCTACGATGTCAGA
CAAAGAAGGGATCCAGCTCTGAATACACATGGTTAAGGATGGCATCGTTGCTAGAAA
ATCCCCAGACTGGCTCCAAACACCAACAGCTCATACACAAATGAATAACAAACTGGA
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAAATTCTGTGAAGCCCGCAATT
TGGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCGTAGTAGTTGTGGCTTAGTGATTCCGTTGTGGCTTGTTGCTAT
GCTCAGAGGAAGGCTACTTTCAAAAGAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGGAAATGTGCAGTGCTCACGCCGTAAATCCCAGCACTTGGAGG
CCGGCGGGCGGATCAGGAGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTAAACCC
CATCTCTACTAAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAACACTGAAACCCGGAGGGGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAAACAGAGCAAGATTCCATCTCAAAAATAAAATAAAATA
AATAAAATAGCTGTTTACCTGAGATTCTACAATAATAGCTGATATT

FIGURE 24

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGI
RLLENPRLGSQST
NSYTMNTKTGTLQFNTVSKLDTGEYSCEARN
NSVGYRRCPGKRMQVDDLNISGIIAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSKATTMSENVQWLTPV
IPALWKA
AAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTTAACATGCTCCACGCCGGACCTGGCAT
CATGCTGCTATTCTCTGCAAATACTGAAGAAGCATGGGATTAAATTTACTCTAAATAA
ATGAATTACTCAATCTCTATGACCCTATACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTTCTCTCTTCAATATGCACTGACATTGGAGAATG
CAATTGTGCACTGCACTTATTCTCAGTAAGGAAACTTGTGGTTCTATGGCATTCTCATCA
TTTGACAATGCAAGCATCTCTTCTTCAATCAGCTCTTGAACCTACTAGCACTGACTG
TGAATCTTAAAGGGGCCATTCTTCAAGAAGAAAGCTAAGATGAAAGGACATGCCACT
CGAATTCTATGTGCTACTTGCCCTAGCTATCACTACACTAGTACAAGCTGTAGA
TGGATTGTCCACGGTTATGACGTGTGAATCAGGCCCTGGTTACACCCAGATCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTCTCAGACATCAAAATATTGCAAAATATTGAAATACTCCACAG
ACTTCCAGTAACCTTACTGGCTCTGGATTATTCTCAAAACAAATTATCTTCACTGACCAAT
ATAATGTAAAAAGATGCCCTAGCTCCTTCTGTGTACCTAGAGGAAACAAACTTACTGA
ACTGCCAAAGGAAATGCTGTGCGAACACTGCAACTTAAAGAAACTCTATTAATCACAACT
TGCTTTCTCAATTTCACTGGCAGGCCCTTATGGCTCACATAATTCTTCTGACTTCATCTC
AATTCAAATAGATTGCAAGATGATCAACAGTAAGTGGTTGATGCTCTTCAATCTAGAGAT
TCCTGATGATTGGGAAATCCAATTATCAGAATCAGAACATGAACTTTAACGCTTATCA
ATCTTCGAGCCTGGTTATAGCTGTAAACCTCAGGAAATACCGATAACGCCCTGGTT
GGAACCTGAAACACTTAGAGAACAGCTCTTCTACAGATAACAGCCTTATTAAAGTACCCCATGT
TGCTCTTCAAAAAGTGTAAATCTCAAATTGGATCTAAATAAAATCTTATTAGAA
TACGAAGGGGTAGTTAGCAATATGCTACACTTAAAGAGTTGGGATAAAATAATGCT
GAGGCTGATTTCATCGATAGTCTGCTGTGGATAACCTGGCAGAGTTAAAGAAAATAGAAC
TACTAACACCCCTAGATTGCTTACATTCAACCCCAATGCATTTCAGACTCCCAAGCTGG
AATCACTCATGCTAACAGCAATGCTCTCAGTGGCCCTGTACCTGTTGACATTGAGTCTCTG
CCAAACCTCAAGGAATCAGCATAACACAGTAACCCCATCAGGTGTGACTGTCTCCTGG
GATGAACATGAAACAAAACACATTGATTGATGGAGGCCGATTCACTGTGTTTGCCTGGACC
CACCTGAATTCAAGGTCAAGATGTTGGCAAGTGCAATTCAAGGGACATGATGGAAATTGT
CTCCCTTCTTATAGCTCTGGAGACTTCTCTTCAATCTAAATGAGGTTAAAGCTGGGAGCTATGT
TTCCCTTCTACTGAGACTCTGGAGAACACCAGCCGTTGAAGAATCTACTGGATAACACCTTCTG
GTCAAAACACTCTGCTTAACCTGACAGACAAGTTCTATGTCATTCTGAGGAAACACTA
GATATAAAATGGCGTAACTCCAAAAGAAGGGGTTTATATCTACTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAACTGTGTTATGATCAAAGTGGATGGATCTTTCACAAAGATAAACATG
GCTCTTGAATTTAAAGAGATATTCAAGGCCATTCACTGTTGGTGTCTGGAAAGCA
AGTTCTAAAATCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGCGAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTTGAGTAAATTGTTGATGATATTCCCAACCATCTATCAGAAAAACAGAAAAAA
TGTGTAATGTCAACCAACCAAGGTTGACCCCTGATCAAAAGAGTATGAAAAGAATAATAC
CACACACACTTATGCCCTGCTTGGAGGCTCTGGGATTATTGGTGTGATATGCTTATCA
GCTGCTCTCTCCAGAAAATGAACACTGAGTGGTGGACACAGCTATGTGAGGAAATTACTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGTAAATCTCTGGAAAGCAGGAAA
AGAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTACCAACAAATATGCTCC
AAAAACCAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLLQTNNIAKIEYSTDFPVNLTGDLQLSQQNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELNLQELYIYHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDAL
LPNLEILMIGENPIIRIKDMNFKEPLINLRSVIAGINLTERIPDNALVGLENLESISFYDNRL
IKVPHVALQKVVLKFLDLNKPNIRRGDFSNMLHLKELGINNNPELISIDS LAVDNLPD
LRKIEATTNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGGLYTC
IATNLVGAIDLKSVMIKVDGSFPQDNNGSLNIRKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARIPSDVKVYNLTHLNPESTEYKICIDIPITYQKNRKKCVNVTTKGLHPDQKE
YEKNNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDDGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GC CCGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGAATTGTCGACATTCCAGCATGAATCT
GGTAGACCTGTGTTAACCGCTCCCTCCATGTGTCCTCTACAAAGTTGTTCTTA
TGATACGTGCTTCATTCTGCCAGTATGTGTCCTAACGGGCTGTCCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCACGGCATTGAGTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCAAAATGCTTCATAAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGACATGGCGTCAATCATGAGACAGCCAC
AACGTGATCTGTAACAGTCCGTGTTGGATGAAACATGCTGGCAGACCTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCCAAATCAGGAG
GATGCCCGAGACACCTCGAATACCTGAAATCCCTGCCAAGCAGGCCAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTTGTAATGTGTCAAACGTGACTGTGATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAACATTGAA
ACTTTGTATTCAGTTTTTGAAATTGCCACTGCTGAACCTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCACTCTCACTATTAAATGAAATTATTTTT
AATTAAAAGCAAATAAAAGCTTAACCTTGAAACCATGGAAAAAAAAAAAAAAACAA

FIGURE 28

MNLVDLWLTRSLSMCLLQS FVLMILCFHSASMC PKGCLCSSGGLNVTCSNANLKEIPRDL
PPETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSL DNR
IQSVHKNAFNNL KARARIANNPWHCDCTLQQVLRSMASN HETAHNVICKTSVLDEHAGR PFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKF
VAVPEGIPETRRLLDLGKNRIKTLNQDEFASFPHLEELNEENIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPLGVFTGLSNTKQDISENKIVILLDYMFQDLYNLKSLEVGDNLDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGIVLRLRHINNAIRDYSFKRLYRLKVLEISH
WPFYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHIVYLRFLNLSYNPISTIEGSMILHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRLVNVSGNQLTLEESVFHSGNLETLILDSDNPLA
CDCRLLWVFRWRRLNFNRQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNSNGLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCCACGCGTCCGCACCTCGGCCCCGGCTCGAAGCGGCTGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCGGCCGGGAAGCGCGATGGGGGCCAGCCGCCCTCGCTCCCTGCTCCCTGC
TCTTCGCGCTGCTGGCGCCGGCGGGCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGGGCTGGTGCACCGTGGTCAAGTGCCAAAGTGAAAATCA
CGAGGACTCATCCCTGCAATGGTCAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCACTGGTTACCTCTACGCCACAGAGCTCAGCATCAGC
ATCAGCAATGGGCCCTGGCAGCAGGGGAGTACACCTGCTCAATCTTCACTATGCCGT
GCGAAGTCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCTGGTT
ATAAAATCTTCAATTACGGGAAAAGACACGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTACCAAGAACTCCACGGAGAACCAACCCGAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTGGTGAACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATGTTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCAATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCTCGTGGGGCCAGAACGCTGTTGCTACACTGTGAGGGTCCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCA
CAACATGGCAGCTACAAGGCCACTACACCCCTCAATGTTAATGACCCAGTCGGTGCCT
CCTCTCCAGCACCTACCACGCCATCATGGTGGGATCGTGGCTTCATTGTCTCTGCTG
CTCATCATGTCATCTCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAGGCTCCGACGATGCTCCAGACGGGACACGGCCATCATCAATGAGAAGGG
GGCAGTCAGGGGGGAGCACAAGAAGGAATATTCATTAGAGGCGCTGCCACTTCTGC
GCCCCCCAGGGCCCTGTGGGACTGCTGGGGCGTCACCAACCCGGACTTGTAAGAGCAA
CCGCAGGGCCGCCCTCCCGCTTGTCTCCCCAGCCCACCCACCCCTGTACAGAAATGTC
TTTGGGTGCGGGTTTGTACTCGGTTGGAATGGGAGGGAGGGAGGGGGGGGGGGGG
TTGCCCTCAGCCCTTCCGTGGCTTCTCTGCATTGGTTATTATTATTTGTAACAAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGGCAGGCCCTGGGTGAGAAAAGCAAAAAACA
AACAAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFFFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCCACCCCCCCCACCCACCCCTTTCTTCTCCTTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAAATTGTGTCGTCGGCAGCAGGATGGTCGCG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGTTAAAATGCTGTTGGATTCTGTT
GCTGGAGACGCTCTTTGTCGGTCAAACGTTACAGGGGACGTTGCAAAGAGAA
TCTGTTCTGCAATGAGATAGAAGGGGGACCTACAGTGAAGTGTGAAAAAAAGGGCTTCACA
AGTCTGAGCGTTTCACTGCCCGACTTCCAGTTTACCATTTATTCTGCATGGCAATT
CCTCACTGACTTTCCCTAATGAGTTGCTAACTTTATAATGCGGTAGTTGCACATGG
AAAACAATGGCTTCAGTAATGCTCCGGGCTTTCTGGGCTGCACTGGTCAAAGG
CTGACATCAACAACAACAAGATCAAGTCTTCTGGAAAGCAGACTTTCTGGGCTGGACGA
TCTGGAATATCTCAGGCTGATTAAATTATTACAGGATATAGACCCGGGCTTCAGG
ACTTGAACAAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTGCACTACCCACCTGCCACCTCGACCTCCGGGTAACAGGGCTGAAAGCTGCC
CTATGAGGAGGTCTGGAGCAATTCTGGTATTGCGAGGATCCTGCTAGAGGATAACCCCT
GGGACTGACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGAAAACATTCCAAGAATGCC
CTGATGCCGCAAGTGTCTGGCAAGGCCCCAACAGACTGCAAGGTTAAAGACCTCAATGAAAC
CACCGAACAGGACTGTGCTCTGGAAACAGACTGCTGGTATTCTAGTCTCCGGGCCCTG
CCCAAGAAGAGACCTTGTCTGGACCCCTGCCAACCTCCTTAAAGACAATGGGCAAGAG
GATCATGCCACACAGGGTCTGTCACAAACGGAGGTACAAGATCCACGGCAACTGGCAGAT
CAAACATGACCCCCACAGCAGGATAGCGACGGGTAGCTCAGGAAACAAACCCCTAGCTAAC
GTTTACCTCTGCCCTGGGGCTGCACTGCCACCATCCAGGGTGGGTTAAAGATGAAAC
TGCACAAACAGGAACAGTGAGCAGCTGGTGTGTTGAAGGCCAACGCTCTAACGTGAGGA
GCTTTCTCAGAGATAACAAAGATCCACGATGCCAAATCGCACTTGTGGATTAAAGA
ACCTCATTCTGGATCTGGGCAACATAACATCGTACTGTAGAGAAACAACACTTCTAAC
AACCTTTGGACCTCAGGTGGCTATACATGGATACAGCAATTACTGGACACGGCTGTCCGGGA
GAAATTGCGGGCTGCAAACCTAGAGTACCTGAACTGGAGTACAACGCTATCCAGCTCA
TCTCCCGGGCACTTCAATGCCACATGCCAAACTGAGGATCTCATTCACAAACACCTG
CTGAGGTCTCTGGTGGACGTGTTCTGGGCTCTGCTCTCAAACCTAGCGCTGAGGA
CAATTACTCATGACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCATCCAGA
TAGACCTCCAGGAAACCTGGAGTGTCTCTGCAACATTGTGCGCTTAAAGCAGTGGGCA
GAACGCTTGGGGTCTCGAAGTGTGATGAGCAGCTCAAGTGTGAGACGGGGTGAACCTT
TAGAAAGGATTCTATGCTCCTCTCAATGACGAGATCTGCCCTCAGCTGCTAGCTAGGACT
CGCCCACTGTTAACTTGCACAGTAAACAGCCTGGGTGGGGAGACGGGGAGCACTCC
AACTCTTACCTAGACACAGCAGGGTGTCCATCTGGTGTGGTCCGGGACTGCTGCTGGT
GTTTGTCTCTCCCTCTCAGCTGGTGGCATCTCGTTTACCTGAGGAACCGAAAGC
GGTCAAGAGAGAGATGCCAACTCTCCGGTCCAGGATTAATTCCCTACAGACAGTCTGT
GACTCTCTCTACTGGCACAATGGGCTTACAACGCAAGATGGGGCCACAGAGTGTATGACTG
TGGCTCTCACTGCTCTCAGATAAGACCCCAACCCAAATAGGGAGGGAGAGGGAGGGC
ATACATCTTCCCCACCGCAGGCCACCCGGGGCTGGAGGGGCTGTAACCAAATCCCCCG
CCATCAGCCTGGATGGGCATAAGTAGATAATAACTGTGAGCTGCCACAAACGAAAGGGCT
GACCCCTTACTTAGCTCCCTCTGAAACAAAGAGCAGACACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTGCTCTTGTGCTAGAGGCCCTTGTGACAAAGCCAGCAGCACCCCTGCTGGAG
AACTGACAGTGGCCCTGCCCTGGCCCCGGGCTGTGGGGTGGATGCCGGTTCTATAC
ATATATACATATACACATCTATATAGAGAGAGATGATATCTATTCTCCCTGTGGATTAG
CCCCCTGATGGCTCCCTGTTGCTACGCAAGGATGGCAGTGTGACAGAAGGATGAATGTAT
TGTAAATAAGTAACCTTGTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTVGDVCKEKICSCNEIEGDLHVDCCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFNEFANFYNAVSLHMENNGLHEIVPGAFQDNLNKLEVLIILNDNLISTLPANVFQYVPITHDLRG
NRLKTLFPEEVLEQIPGIAEILLEDNPWDCTCDLSSLKEWLENIPKNALIGRVCCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLAPPQETFAPGPLPTPFKTNQEDHATPGSAPNGGT
IPGNWQIKIRPTAAITGSSRNKPLANSLCPGGCSDHIPGSGLKMNCNNRNVSSLADLK
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIAVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNBYNAIQLLPGLPTFNAMPKLRILILNNNNLRLSPVDFVAGVSL
SKLSLHNHYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLSMSLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL
VPGLLLTVFTSAFTVVGMLVFLRNRKRSKRRDANSASEINSLQTCDSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577, 608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349, 354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCGTGACCCGGCGCCAGCTGTGTTCTGACCCCAAGAATAACTCAGGGC
TGCACGGGGCTCGCAGCGCTCGCACACATTCTCTGCGGGCTAAAGGGAAACTGTGGC
CGCTGGGCCCCGGGGGGATTCTTGGCAGTGGGGGGCTCGTGGGAGCGAGGGCGGGAGGG
AAGGGAGGGGGAAACGGGGTGGGGAGGCCAGCTGTAGAGGGCGGTGACCGCCTCCAGACAC
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGGGGGCTCGCTACAGCGTC
AGAATGAGGCCCGCTTCGCCCCGTGCTCTCTGCGCAGGGCCTGCCCCGGGGCGGG
CGGCAGAACACCCCCACTGCCGACCGTGTGGCTGCTCGGCTCGGGGGCTCGCTACAGCGTC
ACACCGCTACCATGAAGCGGAGGCCAGGGCTGCACTCTGCGAGGTGGGGCGCTC
AGCAGCGTGTGCGGGCGCCAGCTGCGCCTGTGCTCGCCTCTGCGGGAGGCCAGG
GCCGGAGGGGCTCAAAGACTGTGTTCTGGGCGCACTGGAGCGCAGGGCTTCCACT
GCACCCCTGGAGAACGAGCCCTTGGGGGTTCTCTCTGGCTGTCTCCGACCCGGCGTCTC
GAAAGCAGAACCGCTGGAGGGGGCCAAACGCTCTGCAACGGCCGGAGATGCGC
GGTACTCCAGGGCACCGGCTGGGTCGAGGCCCGCAGCTGGAAGGAGATGCGATGCCACCTGC
GCCAACCGGCTACCTGTGCAAGTACCAAGTTGAGGTCTGTGCTCTGCGCCGCCCCGG
GCCGCTCTAAGCTGAGCTATGCCGCGCCCTTCACTGCAACAGCGCCCTCTGGACTTCA
TCCACCTGGGAGCGAGGTGAGTGTGCGCTTGGGGGACAGCTCCGATCTCAGTTACTGCA
TCGCGGACGAATCGGCGCTGGGACAAACTCTGGCGATGTGTTGTGCCCC
GGGAGGTACCTCTGGCAATGCGAGAGCTCCCTAAGCTGCTAGACGACTTGGGAG
CTTGGCCTGCGAATGTGCTACGGGCTTCAGCTGGAGCTGGGGAGGACGGCCGCTTGTGACCA
GTGGGGAGGACAGCCGACCTTGGGGGACCGGGGTGCCAACCCAGGGCGCCGGGCACT
GCAACCCAGCCCCGTGCCGAGAGAACATGGCAATCAGGGTGCAGGAGCTGGAGAGAC
ACCACTTGCTGCAACAGAACATACTGACATCTTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGCTTCAAGGGCAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGAATTCCAAGTTAATTCTACGACTTCTGCACTCTCAGGTTT
CGACTCTCTCTGCGCTGTCTCATATTGTGAGCACAGCAGTAGTGTGTTGGTGTACT
TGACCATGACAGTACTGGGGCTTGTCAAGGCTGCTTACGAAAGGCCCTTCCCAGCCA
AGGAAGGGAGTCTATGGGGCCGGGGCTGGAGAGTGTACCTTGAGCCCTGCTTGGGCTC
CAGTTCTGCACATTGCAACAAACATGGGGTGAAGAGCTGGGACTGTGATCTGGGAGAG
CAGAGGGTGCTTGTGGGGAGTCCCTTGGCTCTAGTGTGATGCAATTGGAAACACAGGG
CATGGGCACTCTGTGAACAGTTTCAATTGTGATGAAACGGGGAAACCAAGAGGAACCTAC
TTGTGTAACTGACAATTCTGAGAAATCCCCCTTCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAAACTGACACTCTTCCCTGTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGTCATACTGGGGGACGGGTAGTGTGCTGGGGAGAGATATTCTTATGTTATTGGAGA
TTTGAGAAGTGATTGAACTTTCAAGACATTGAAACAAATAGAACACAAATATAATTACA
TTAAAAAAATATTCTACAAAATGAAAGGAAATGTTCTATGTTGTTAGGCTAGGAGTAT
ATTGGTTGAAATCCAGGGAAAAAATAAAAAATTTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPAGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVIALLRAAGPGPGGSKDLLFWVALERRSHCTLNEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCSTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPG
ASNLSYRAPFQLHSAAALDFSPPGTEVSALCRGQLPISVTCAIDEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVQORTWPIRDEKLGETPLVPEQDNSTVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIIVFSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDEPEAALGSSAHCTNNGVKVGDCDLRDRAGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTCAAGCTGGCCCTGTGGCTGCCAGAGCAGCTCTCAGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATACTGCCCTTAAAGTCCTCCGCCCTGCCGGCGCTATC
CCCCGGTACCTGGCCGCCCGCGCGGTGCGCGCTGAGAGGGAGCGCGCGGGCAGCCGA
GCCGCCGTGTGAGCCAGCGCTGTGCGAGTGTGAGCCGCGGTGTGAGCCGCGGGTGGTCCGA
GGGGCGTGTGCGCCGCCGCCCGCGGTGAGGGAGCGCGCTACGCTGCCATGA
GGGGCGCGAACCCCTGGGCCCACTCTGCCCTGTGCTGGCTGCCCAACCCAGCTCTCGGG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCGGATT
TATTGGCAGTGAGGTTTCCCTGGAGTCACCTCCAAATGCAAATGTACTTGGAAAATCA
CAGTCTCCGAAGAAAAGTAGCTGTTCTCAATTCCGATTATAGACCTCGAGAGTGACAAAC
CTGTGCCGCTATGACTTGTGGATGTGTAACATGCCATGCCATGCCAGCGCATTGCCG
CTTCTGTGCCACTTCCGGCTGGAGGCCCTGTGTCAGTGGCAACAAGATGATGGTCCAGA
TGATTTCTGATGCCAACACAGCTGCCATGCTCATGCCATGTTCTCCGCTGCTGAACCA
AACCAAAGAGGGATCACTATTGAGGACTCTTCGACAGCCTTCCGGCTCTTTAAAC
CCCAACTGCCAGACCGGGATTACCCCTGAGGAGTCACCTGTGTTGGCACATTGAGCC
CAAAGAATCAGCTTATAGAATTTAAAGTTGAGAAGTTGATGAGGAGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCACCATGCTAGAGAATTGAAA
GTATTGTGGTGTAGTCACCTGCGCCAATTGTGTCAGAGAGAAATGAACCTCTTATTGAGT
TTTATCAGACTTAAAGTTAACTGCAAGTGGGTTATTGGTCACTACATATTCAAGGCAAAA
AAACTGCCCTACAACTACAGAACAGCCTGTCACCCACATCCCTGTAACCACAGGGTTAAA
ACCCACCGTGGCCTTGTCAACAAAAGTGAGCAGGACGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTGTATTAGCCGGACTGTGTTATCACACCATCACTCGCGATGGGAGTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATTTCAGCAGCGGG
CAAGAACATGACTGCCAGGCTGACTGTGCTGCAAGCAGTGCCCTCTCCAGAAGAGGTC
TAAATTACATTATTATGGGCAAGTAGGTGAAGATGGGAGGGCAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAAATCAGAAGGCTCTGGATGCCCTTAAAATAAGCAATG
TAACACTGAGACTGTGTCATTAAAGCTGTATTCTGCCATTGCTTGAAGATCTATGTT
TCTCACTGAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTTCACTGATGGGGTATGAGGCCCTCCGAGATAGCTGAGGGAACTTCTT
TGCCTGCTGTCAGAGGAGCAGCTATCTGATGGAAACCTGCGGACTTACTGCGGTGATAGGA
AGCTAAAAGTCAGCGTGAAGCTGGAAAGCGTTTATTTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTTGTAAGATGTCAAAAAAAGATTAGAAGTGCAATATTATAGT
GTATTGTGTTTACCTTCAGGCCATTGCCCCGAGCTGTTAACATCTGTCTTGCCTTCTA
AACTCAATGCTTAAATAAAATTTTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESIDLNCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCACCAGGGCTGGGCGGTGCGCTTCTT
CCTCTCCGTGGCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTCATACTG
CCGGGACTGGTGACAGCTTAACAAGGGCCTGGAGAGAACATCCGGGACAACCTGGAG
GTGAAACACTGCTGGAGGAAGAGAAATTGTCAAATACAAAGACAGTGAGACCCGCTG
GTAGAGGTGCTGGAGGGTGTGAGCAAGTCAGACTTCGAGTCCACCGCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTACAAGCAGCAGGAGGCCGACCTCTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCAGGGCCCTCTGC
CTTCCCTGCTCTGGGGAAACAGAGGGCCCTGCGGTGGTACGGGAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGCCACTGTGACTGCCAACGGGCTACGGGGTGGAGGCCCTGCGC
AGTGTGGCTTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACCTGTTGCAATGCAAGAAGG
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCAAGAGGGAGCCAAC
GTGGAGCTGACCAATTCTGCGTAACACTGAGGGCTCTATGAGTGCCGAGACTGTGCCAAG
GCCGCTTAGGCTGCATGGGGCAGGGCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCAAGTGTCTGATGTTGAGTGTGAGACAGAGGTGTGCTGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGTGCATCTGTGCCAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGCCA
CGCTGGCTGCTAAGGGCAGTTGGTGTACCGCCATCTTCAATTGGGCTGTGGGGCCATG
ACTGGCTACTGGTTGTCAAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGAT
ATCGCGGCCACCCACCTGTAGGACCTCTCCACCCACGCTGCCAGAGCTGGGCTGCC
TCCGCTGGACACTCAGGACAGCTTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTTCAACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCCTCACAGGGGTGGGCCATCACGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTCACACATCCCCACCCCCATTGCCACTTATTATTCATCTCAGGAAATAAGA
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWVFHKQ
QEAPDLFWQLCSDSLKLCCPAGTGFGPSCLPCPGGTERPCGGYGGQCEGEGTRGGSGHCDCQAG
YGEACCCQCGLGYFEAERNASHLVCSACFGPCARCSGPESNCLQCKKGWALHHLKCVDIDE
CTEGANGCADCQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCNTEGGYRCIAEGLYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLRSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-363

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCCTCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCCTTGCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCTGGGAGCAGCTGCCAGCTGCCAGCTGAGCTAAAGAGGT
GCCCACCCCTGGACAGGGCCGACATGGAGGGACTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCACGGGACCGCTCCCGGGAAAGGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCCTGGAGGCCAGCACACACTGCTGGTGGTCCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGAGGCCGCTGCCGCTCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCCGTGTCCCCGCCAGCGCCGGGCC
CGGGTGACCGTCGAGTGGCTCGCGTCCGGACGACGGCTCCAACCGCACCTCCATCGA
CTCCAGGCTGGTGTCCGTCCAGAGAGCGCTGGAAAGGCCCTCGACGTGACCGAGGCCGTGA
ACTTCTGCAGCAGCTGAGCCGCCCGGAGCCGCTGCTCACAGGTGTGGTCAAGAGG
GAGCAGCTGGGCCGCTGGCTCGGCCAACAGCTGGTCCGCTTGCTCGCAGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCACATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACACTGGGTGCTGGAGCCCCCGGCTT
CCTGGCTTATGAGTGTGACCGGACCTGCCGGCAGCCCCGGAGGCCCTGGCCTCAAGTGGC
CGTTCTGGGCCCTGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAAGCCCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCCTGGATGGTGCCTGCAAGGAGGCTCCAGCCATAGGCGCTAGTG
TAGCCATCGAGGGACTTGACTGTGTGTTCTGAAGTGGTCAAGGTTACCAAGGAGAGCTG
GCGATGACTGAAGTGTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTGGCTTCTCAGGAATGAGAACATTGGCCACTGGA
GAGCCCTGCTCAGTTCTTCTATTCTTACTGCAACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCTGTCATTGTTACTTGCTGTGAC
TGGATCTGGCTAAAGCTCCACCACACTGGACCTAACAGACCTGGGTTAAGTGTGGGT
TGTGATCCCCAATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSSLRQLQLKEVPTLDRADMEELVIPHVRQAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRVDDGSNRRTSLIDSRLVSVHESGWKAFDVTTEAVNF
WQQLSRPRQPLLLQVSQREHLGPLASGAHKLVRFASQGAPAGLGEQPLLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFWKPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVS LPNMRVQKSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTCAGTGGCCTGATCCGGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTCCTTCAATTGGCATCCGTTGCTCCCTGG
CATTGGCAGTGTACAGTGCACTCTTGAACCTGAAGTCAGAATTCTGAGAATAACCT
GTGAAGTGTCTGCTACTCGGGCTTCTCTCCCGTGTGGAGTGGAAGTTGACCA
AGGAGACACCACCAGACTCGTTGCTATAAAACAAGATCACAGCTCTATGAGGACCGGG
TGACCTTCTGCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGAACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT
GCTCTGCTCCATCCAAGCCTACAGTAACATCCCTCTCTGCCACCATGGGAAACGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTTCTGAATACACCTGGTCAAAGAT
GGGATAGTGATGCTCACGAATCCAAAAGCACCGTGCTTCAGCAACTCTCCTATGTCCT
GAATCCCACAACAGGAGACCTGGCTTGTACCCCTGTCAGCTCTGATACTGGAGAACACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCCTGTAACCCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCCTATAGCGAGGCCACTTGACAGAACAAAGGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCACCTAGTGCCGAAGTGAAGGAGAACAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGTCGCTACCGCCTATCATCTGCATTGCTTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCGTGTTACAGGATGCCTTATTGCTTC
TACACCCACAGGGCCCCCTACTCTCGGATGTGTTTAATATGTCAGCTATGTCCCCC
ATCCCTCCTCATGCCCTCCCTTCCTAACACTGCTGAGTGGCCTGGAAACTGTTAAA
GTGTTTATCCCCATTTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCC
TTCTAAGTAGACAGCAAAATGGGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTGAGCTTGGTCTGGCTTCTTGATGTACTGAC
GACCAGGGCCCAGTGTCTAGAGCGGGAAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGTCTTCCATCTGGGCCACTCTTCTGTCTTCCATGGGAAGTG
CCACTGGGATCCCTGCCCTGCTGCTCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAATGGGAGCTTGTGAGAGCATAGAAATTTCAGAGAACCTGAAGGCAAAAG
GATTAAAACCGCTGCTAAAGAAAAGAAACTGGAGGCTGGCGCAGTGGCTACCGCTG
TAATCCCAGGGCTGAGGCAGGCGGATCACCTGAGGTGGGGAGTTCGGATCAGGGCTGACCA
ACATGGAGAAACCCACTGGAAATACAAAGTTAGCCAGGCCATGGTGGTCATGCCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSAYSGFSSPRVEW
KFDQGDTTRLVYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGN SYGEVKV
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPSEYTWFKDGI VMPTNPKSTRAFSNS
SYVLNPTTGEVLVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCTGGCGCTGCTGCTGCTCGCTCGGACTAGGCCT
GGAGGCGCCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGGCCAGCTAG
GCTCGTGCACCCACCAAGTCCAGTGCCTGCGACCAGTGGCTTATGCGTGCCCCCTACCTGG
CGCTGCGACAGGGACTTGGACTGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACGCCCTGGCTCCCTGCCCTGCACCGGGCTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCGAGGCCCTGGCTGCCTAGCA
GGCGAGCTCCGTTGACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGAGCTGGCTGTGGAACCAATGAGATCCCTGGGAAG
GGGATGCCACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTGGGAATGCCACATCTC
CTCTGCCGGAGACCAGTCTGGAAAGCCCAACTGCCCTATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTGCAGCCTGGTACCGCCACCCCTCCCTTGTCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCCACTGGGTTACTGGTGGCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAC
CTCGCTGCCCTTGAGGACAAGCAACTTGCACCCACCGTCACTCAGCCCTGGCGTAGCCGACA
GGAGGAGAGCAGTGTGGATGGTACCCGGCACCCAGCCCTCAGAGACCTGAGTTCTT
CTGGCACGTGAAACCTCGAACCCGAGCTCTGCGAGAAGTGGCCCTGGAGATTGAGGTCCC
TGGACACTCCCTATGGAGATCGGGGAGCTAGGATGGGAAACCTGCCACAGCCAGAAC
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCGGTDKKL
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPTVLESVPVGNAATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSPLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACACGCGTCCGGTCTCGCTCGCTCGCGCAGCGCGGCGCAGCAGAGGTCGGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAAGGAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGAACATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTCAAGCTGGCTGTGCTTCGGCCCTGCACAGCTCACGGGGGTT
CGATGACCTCAAGTGTGTGTCGACCCGGCATTCGGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTTCACTGCAAGACGGATTCAAGCTGAAG
GGCGTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAAGTGA
TAATTCCATCTGTGCAAGAAGATTGGCTATCCCTAAATCGAAGATGCTGAGATTCTATA
ACAAGACATATAGACATGGAGAGAAGCTAACTCATCTTGTGTCATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCAATTGTGGCATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCTCTTCAATGGCTATGTAACATCTGTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCTATCGCTGCTTCCGGATTTAAACTT
GATGGGTCTGGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCAGCCCACCCGGTG
CCTTGCTCTGGAAAGCCAACTGTGTCACCTCAATGGTAGTCACTGGAGATTCTGTCT
GCCACCCCGCCCTTGTGAGCGCTACAACCAACGGAACTGTGGGGAGTTTACTGCGATCCT
GGTACAGCCTACCAGCGACTACAAGTACATCACCTGCAGTATGGAGAGTGGTTCCCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAACAGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCTTCACGGCAACCAGTGTGCTGCTGGTGTGCTGCTGTCATC
CTGGCAGGATGTTCCAGACCAAGTCAAGGGCACTTCCCCCCCAGGGGGCTCCCCGGAG
TTCCAGCAGTGACCTGACTTTGTGGTGGTAGACGGCGTGCCCCGTGTCATGCTCCGTCATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCCGGTACATGGCCTCTGTGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGGACAGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTTCTGAGCTGCTCCAAA
GTCTGTATTCACTCCCAAGGTGCAAGAGAGCACCCACCTGCTCGGACAACCCCTGACATA
ATTGCCAGCAGGCCAGAGGGAGTGGCATCCACCAAGCCAGGAGCATCCATGCCCCACTGGT
GTTGTTCTAAGAAACTGATTGATTAATTTCCAAAGTGTGTCATGAGTGTCTCTCAA
ATACATGTTGATCTGTGGAGTTGATTCTCTCTTGGTTAGACAAATGTAAACAA
AGCTCTGATCCTAAATGCTATGCTGATAGAGTGGTGAAGGCTGGAAGCTTGATCAAGTC
CTGTTCTCTTGACACAGACTGATTAAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKAGTKRLCLKHFNGLTGWI PSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKITYTCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDI IASTAEEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACACGCGTCCGCTCCGCCCCCTCCCCCGCCTCCCGTGCAGGTCCGTCGGTGGCCTAGAGA
TGCTGCTGCCGCCGGTTGCAGTTGTCGCGCACGCCCTGCCGCCAGCCCGCTCACCAGCGT
AGCGCCGAGTGTCCGGGGCGCACCCGAGTCGGGCCATGAGGCGGGAACCGCGTACAGG
CCGTGCTGCCGTGCTGGGTGCTGGTGGGCTGCCGCCGACGGTCGCCCTGCTGAGTGC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCCTGTTA
TAAAGTCATTACTCCATGATACTCTCGAAGACTGAACATTGAGGAAGCCAAAGAACGCT
GCAGGAGGGATGGAGGGCAGTCAGTCAGCATCGAGTCTGAAGATGAACAGAAAATGATAGAA
AAGTTCATGAAAACCTTGCATCTGATGGTGAATTCTGGATTGGCTCAGGAGGCGTGA
GGAGAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGACTGATGGCAGCATAT
CACATTAGGAACCTGGTATGGATGAGCGTCCTGCCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCCTGGCATCGAGGCCCTACATGTTCACTGGAAATGATGA
CCGGTGCAACATGAAGAACATTCTGGATTGAGAACACCAGCAGTCCCT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAACACAG
GAAGAACAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCCTGAATCTGCCCTACAT
CCTAATCCCCAGCATTCCCTCTCCCTCTTGTGCTCACAGCTTGTATGGTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAGAACACACCATC
TGGCCCTCTCCTACCAGGGAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAACGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTCTGGAGTGTGTT
CGGGAGAACCCACTCCCGATGACATGCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTGTGACTCTGGTGGAGACTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAAATGGGAGGGACTAAGGAGTCTGGATGGTGGAAAATGAAATATG
GTATTAGGACATAAAAAAACTGAAACTGACAACATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGGAAAATACACAGAAGGTCTATGAAACAGCTTAGATCAGGCTCTGT
GGATGAGCATGTGGTCCCCACACCTCTGGACCTTGGACCCCCACGTTTGCTGTATCCTTAT
CCCAAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCATTGGTTGGTTGATCTAACTTTAACGGGACAGAGCTTACCTG
GCAGTGTAAAGATGGGCTGGAGCTGGAAAACACCTCTGTTCTGCTCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAGGCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTCAAAGAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEAKEACRRDGGQLVSIESEDEQKLIKEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAGEEETELTPVLPTEETQEDAKKTFKESREAALNLAYILIPSIPLLLL
VTTVVVWVWICRKRKREQPDPSTKKQHTIWPSHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLVSVESGFVTNDIYEFS
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGGGACTTGGGGCGCCGCTGAGCCCCGGGCCAGAAGACTTGT
GTTGCCTCCTGCAGCCTAACCCGGAGGGCAGCAGGGCTTACCAATGATCACTGGTGT
GTTCAGCATGCCTGTGGACCCCCAGTGGCGTCTGACCTCGCTGGCTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTGCACCGCAGC
CTGCTGAAGTTGAAATGGTCAGGTCTGTTGACACGGGCTCGGAGTCCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTGGAGAGAGACTGAGGAAGAACTATGTTGAGACATTCCCTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTAACTGTTCCACTAACATTTCGGAATCTG
GAGTCACCCGGTTGTTGCTGGCTGGGCTTTCCAGTGTCAAGAAAGAAGGCCATCATCAT
CCACACTGATGAAGCAGATTCAAGCTTGTATCCAAACTACCAAAGCTGCTGGACCTGA
GGCAGAGAACCAAGAGGCCGGAGGAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTCATCCCT
GGACAACGTGGCTGCCAGCAGCACACACCTCCAAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCCTGTACATACTGCCAAGGAAGCAGG
GAAAGTCTCAGATGCCAGTAGGCCATTCCCTCACATCCTAGAGAGCAACCTGCTGAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCCGCTCATGATG
TGACCTTCATACCGCTTAAATGACCCCTGGGATTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGAAACTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTCAGCTCTA
TTACACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTTACCTTAAGCCCAGAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGAAAGTTGGAAATGAAGAGATGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTINLAGGPKPYSFYDSQYHETTLKGGMFAGQL
TKVGMQOMFALGERLKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRRRQTAISLQPGISEDLKKVKDRMGIDSSDKVD
FFIILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYIILPKEDRESLQMAVGPFLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPIIIMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPIDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGAGCTAAACTAAATATTGCTGCTGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGCTCTGCTATTCTCCTGATCCTT
GCCATTTCGACCAGACCTGGATTCTAGCGCTCCATCTGGAGTGCGGCTGGTGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCAGTGGGACCGTGTGATG
ACGGCTGGACATTAAGGACGGTGGCTGTGTTGCGCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAACAGATACTGGCTCAGTGTGAGCAAGAAGATTATG
ATTGTTACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGGCCCTGGGATCTGCAAGGGACGCGTGGAAAGTGA
GCACCAAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGCCTCGGGCGCAAGGTGG
TGTGCCGCAGCTGGGATGTGGGAGGGTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCTAGGACGAGAACCCCTCA
GGATTGCCCTCTGGGCCTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGTCG
AATGTGAAGATCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGCAACAGGGCGTATGGGCTCTGCTGTGATGACAACGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCTCTCCTCCCTGAGAACCGGA
AATGCTATGCCCTGGGGTTGCCGCATCTGCTGGATAATGTTGCTCTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGCACAGATTTGGGGTTTACGACTGCACCCACCAGGAAGA
TGTGGCTGTCTGCTCAGTGATGGGGCATCATCTAATCTGTTGAGTGCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGCTACATGACTGCATGGGATGAACACTGATCT
TCTCTGCCCTGGACTGGGACTTAACTTGGTGCCTGATTCTCAGGCCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGAAACTACATCA
CCACCTTCCTATGTCCTCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTTGAT
CAACTACTTAAACATTCAC
CACCAATTGTCCTGTTCTGTAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACCGAATTAAAGGATAATTCTGTAATTGGTTATGGGTTCTGAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTACAATAATAAGATAGCAC
TATGTGTTAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVL
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCCRAVL
TQKRCNKHAYGRKPIWLSQLMSQSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCGSRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL
DNVRCSGEEQSLEQCQHRFWGFDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTGACCTCGAC
CCACCGTCCGGACCGTGGCGGACCGTGGGCCGCTACCAAGGAAGAGTCGCCAAG
GTGAAGGCCATGACTTCATCACCTCACAGCCATCCTGCCCTGCTGTTGGCTGCCGG
CGTCTTCGGCCTCTCCGGCTGCTGCAGTGGTGCAGGGGAAGGCCACCTGCCGGATGCTG
TGGTGGTATCACAGGCCACCTCAGGGCTGGCAAAGAAATGTGAAAGTCTTCTATGCT
GCCGGTCTAAACTGGTGTCTGTGGCCGAATGGTGGGCCCTAGAAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGG
TGTGGACAAGAGGGTATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC
TGCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTGCGTGGCAGATGAAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCAACACAGGCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGTGCTGTGG
GAAGAAGAAGAAAGATGTGATCTGGCTGACTTACTGCCTTCCTGGCTGTTATCTTGA
CTCTGGCTCCGGCTTCTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGACTCTGACCAGCCAGGGCAGGGCAGAGAACGAGCAGCACTTTAGGTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTAAATGGAGATTGTCTCACAAGTGG
AAAGACTGAAGAACACATCTGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACA
AGCTTCTTCCCAGGGTGGAGGGAAACACTTAAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAAATAAACATCTCAAACAGTAAAAAAAAAAAGGGCGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCAACTTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKEAKVFYAAGA
KLVLCGRNNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAELQCFGYVDIL
VNNAGISYRGTIMDTTVDVDRVMETNYFGPVALT
KALLPSMIKRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLA
AVGKKKDVL
ADLLPSL
AVYLRT
LAPGLFFSL
MASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

FIGURE 58

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIQLTAYEFAKLKSK
LVLWDINKHGLEETAACCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCGTCGGCGGACCGTGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCGACTGCGCCGACCCCTGAGAGATGGTTGGTGCCTGTGGAAGGTGATTG
TTTCGCTGGTCTGTGATGCCCTGGCCCTGTGATGGGCTGTTCTGCTCCCTACAGAAAGT
GTTCCATGCCACCTAAGGGAGACTCAGGACAGCATTATTCCTCACCCCTTACATTAAGC
TGGGAAGATCCAAAAGGGAAAGAGAATTGAGTTGGTCCGGCCCTTCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCTCCTACCCGTGAATAAGACTTACACAGCAACCTTCTCTGGTTC
TCCCCAGCTCAGATACAGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGGG
AGGTTCATCCATGTTGGACTCTTGTTGGAACATGGGCCATGTTGTCACAAGTAACATGA
CCTTGGCTGACAGAGACTCCCTGGACACACAGCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTCAGTTACTGATGATAACCCAGGATATGCACTGAGGACGATGT
AGCACGGGATTATACTAGTGACTAATTCACTGTTTCCAGATATTCCTGAATATAAAAATA
ATGACTTTATGTCAGTGGGAGCTTATGCCAGGGAAATTATGTCAGGCCATTGCAACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGGTTGAAGATCAACTGAAACGGAAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGAGAATTCTGTACCAAATTGGCT
TGGTGGATGAGAAGAAAAAAAGTACTCCAGAAGCAGTGCATGAATGCAAGAACACATC
AGGAAGCAGAACTGTTGGCCCTTGTAAACTACTGGATAAAACTACTAGATGGCGACTTAAC
AAAGTGTACCTTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGGCGT
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTGGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACTATGTTGAAAAGTACTTGGCGAGA
AGATACTAGTACAGTCAGTTAACCCATGGTTACTGAAATCATGAATAATTAAAGGTTCTGA
TCTACAATGGCCAATGGACATCATCGTGGCAGCTGCCCTGACAGCGCTCTTGATGGC
ATGGACTGGAAGGATCCCGAAATACAAGAAGGCAAAAAAAAGTTGGAAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTACATCCGGCAAGCGGGTGAATTCCCATCAGGTAATTATT
GAGGTGGAGGACATATTTCACCTATGACCCCTCTGAGAGCTTTGACATGATTAATCGA
TTCATTATGGAAAAGGATGGGATCCTTATGTTGGTAAAACTACCTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAGAAAATCTAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTCATCAATAAAATTATCCTTGAAACAACTGAGC
TTTTGTTTTGGGGGAGATGTTACTACAAAATTACATGACTACATGACTAAGAATTACA
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAATGA
AATTTTAGGGCTCTGAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAAAGTGCAGTTG
TAACAAACAAAGCTGAAACATCTTTCTGCCAATAACAGAAATTGGCATGCCGTGAAGGT
GTTTGAAATATTATGGATAAGAATAGCTCAATTATCCAATAAATGGATGAAGCTATAA
TAGTTTGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGTAAATAA
AAAATATTATATAAAAGTAAAAAAA

FIGURE 60

MVGAMWKVIVSLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGRELSE
VGPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPyVVTSNMTLDRDRFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLPREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFFEILDKLLDGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGQNQTFNDGTIVEKYLRDVTQSVKPWLT
EIMNNYKVLIYNGQLDIIVAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTCGGCTCCGGAATGGCACATGTGGACCTTCCCAGTCTTGTGGCTACAACAT
TTTCCCCTTCTAAACAAGTCTAACAGCTTCAACAGCTAGTGTACAGGGGTTCTTCTT
GCTGGAGAAGAAAGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCCTT
CCTCTCTGTGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTITGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCTAACAGCTTCAAAAAACAGGAGCAGACTTCACTGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAAGACTGGTTAGTCCTAAATATCAAAATGACTGGCTGGG
TGAACCTCAACAGCCTTTAACCTCTGTGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAAAATTTAAAAAAAGCAATGATTTATAGCATAAAAGGCTAGA
GACCAAAATAGATAACAGGATTCTCTGAAACATCCCTAAGAGGGAGAAAGTATGTTAAAATA
GAAAAACCAAATGCGAAGGAGGAGACTCACAGAGCTAACAGGAGATGGGACCTGGGT
AGGCCAGCCTCTTGCCTCCCGGAAATTATTTGGCTGCAACTCTGCCCTGTGTTT
GCAGAACTCATGTGAGGGGCAACCGGGGAAAGGTGGAGCAGATGAGCACACACAGGGCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGGAGCAGCCCTGGCCCGGCCCTGGAGGTGG
ACAGGCGCTCTGTGGCTCTGCTCATGTGGCTGGGTCTGCTGGCCCCCAGCAGCCGGC
ATGCCCTCAGTTCAAGCCTTCACTCTGAAATGCTGACCTGGACCTTCAACCAACTTGACCGT
CCACCAAGGGAGGGGCCCTGTATGGGGGCAATCACCGGGTCTATAAGCTGACAGGA
ACTGCGACATCAGTGGCTATAAGACAGGGCAGAAGAGGACAACAAGTCTGTTACCG
CCCTCATCGTGAGGGCAGAGCTCCACCTCACCACAAATGTCACAAGCTGCT
CATCATGGACTACTCTGAGAACCGCCCTGCGGCTGTGGAGCCTCTACAGGGGCTGTGCA
AGCTGCTGCGGTGGATGACCTCTTCATCTGGTGGAGCCATCCCCAACAGAAGGAGCACTAC
CTGTCAGTGTCAACAAGACAGGGCACCATGTACGGGTGATTGTGGCTCTGAGGTGAGGA
TGCGCAAGCTCTCATCGGCAGCGCTGTGGATGGGAGCAGGATTCTCCCGACCCCTGTCCA
GCCGGAAAGCTGGCCCGAGACCTCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGGAT
TTTGTCTCCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGGTCTCCACTTGA
CTCTACATCTACGGCTTGTGAGTGGGGCTTGTCTACTTCTCTACTGTCCAGGGCCAGA
CCCCCTGAGGGTGTGCCCATCACTCCCTGGAGACCTCTTCTACACCTCAGCCTGCG
CTCTGCAAGGATGACCCCAAGTTCACTCATACGTGTCCTGCCCCCTGGCTGACCCGGG
CGGGGTGGAAATACGGCTCTGTGAGGCTCTTACCTGCGCAAGCTGGGACTCTACTGGCC
AGGCTTCAATATCACCAGGCCAGGACATGACTCTGGCCCTGTGCTTCTCCAAAGGGCAAG
CAGTATCACCACCCGCCGATGACTCTGGCCCTGTGCTTCTCCATCGGGCCATCAACTT
GCAGATCAAGGAGCGCCCTGCACTGCTTGTACCAAGGGAGGGCAACCTGGAGCTCAACTGGC
TCTGGGGAGGAGCCTGCACTGCAAGGAGCCCTGCTCCACATCGATGATAACCTTCTGTGA
CTGGACATCAACCAAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTAACAGGCTACAGCGTGGTTTGT
TGGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTTCAAGATGCTCCAAATGCC
ATTCACTCTCAGCAAAGAGTCCCTTGTGAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTTATTTCTGGGGACAACAGGTGAATGGGGAGGGTAAGAAGGGTTAATTTCTG
ACTTAGCTCTAGCTACTTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTCACAACTTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSAALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSDRSVVLSSVVVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPPPLIVQPCSEVLTLTNNVNKLIIIDYSENRLLACGSL
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDCKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAAGDLFYTSRIVRLCKDDPKFHYSVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSAACFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTSGKLKKVRYEFRCNSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

FIGURE 64

MTTWSLRRPARTLGLLLVVLGPLVLRRLDWSTLVPPLRLRQLGLQAKGWNFMLEDSTFW
IEFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHUPERGKFDGSGNLDLEAFVLM
AEIGLWVILRPGPYICSEMDLGGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMRSVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAVMPYVKKALEDRGIVELLTSNDKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLNVQGTQPKMVMEYWTGWFDSWGGPHNILDSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLIRDFFGSISGIP
LPPPPDPLLKPMPYEPPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFYIILYE
TSITSSGILSGHVHDRGQVFVNTVSIGFLDYKTTKIAVPLIQQGYTVLRLVENRGRVNYGEN
IDDQRKGGLIGNLYLNDSPLNFKRIYSLDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSLSIS
STPCDTFLKLEGWEKGVVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGGGGAGCTGAGAGGCTCGGGCTAGCTAGGTGTTAGGGTGGACGGGTCGGAGACC
CTGGTGAGGGTCTCTACTTGGCTTCGGTGGGGTCAAGACGCAGGCCACTACGCCAAAGG
GGAGCAAAGCCGGCTGGCCGAGGCCCCAGGACCTCATCTCCCATCTGGAGGAATC
CGACACGTGACCGCTGTCGCCGCTCAGACTAGAGGAGCCTGAAACGCCATGGCTCCC
AAGAACGGTCTCTGCCCTTCTGGCTGCGCTGAGGGTCAAGCCGCTACGCTGACGCTACTGCTGCC
GGCAGACACTCGGTGTTGAGGGTCACTACGCGCTGACTACTTCTGGTACCGCGGTGCTTGGGCC
CGTTCCGCTATGTGCTGGCAGCCTGCACTACTTCTGGTACCGCGGTGCTTGGGCC
CGGCTTTGAAGATGGATGGAGCCCTAACGCCTACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCTGGGTCTATAACTTAAATGGCAGGGGACCTCATGGCTTCTGA
ATGAGGCAGCTAGCGAACCTGTTGGTCAACTAGGACACAGGACCTTACATCTGTGAGAG
TGGGAGATGGGGGCTCCCATCTGGTGTCTCGAAACCTGAAATTCTATCTAAGAACCTC
AGATCCGACTCTCCCTGGCAGCTGGACTCTGGTCAAGGTCTGGCTGCCAAGATATATC
CATGGCTTATCACATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTTCTCGTCACTGCTAGG
AGAAAAGATCTGCTTACACAGATGGCCCTGAAGGACTCAAGTGTGGCTCCCTCCGG
GACTCTATACACTGTAGATTGGCCACAGTCAACACATGACCAAAATCTTACCTCTGTT
CGGAAGTATGAAACCCATGGCATTGTAACACTGTAGACTACACAGGCTGGCTGGATT
CTGGGGCCAGAACATCACTCCACAGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGGAGCCAGTGTGACATGTACATGTTCCATGGAGGATACCAACTTGGATATTGG
AATGGTCCGATAAGAAGGGACGCTTCTCCGATTTACTACAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGACCCACACCTAACGCTTTTGCTCTTGAGATGTCACTGGAACT
TCAGGGAGTTGGGACCTTACCTCCCCGAGCCCCAACAGTGTGGGATTTGGGATTTGG
ACTCTGCACTCTGGGATTGGGCAATTACTGGCTTCTCTAGACTTGTGTTGGCCCGTGGGGCC
TCATTCAATCTGCCAATGACCTTGGAGGCTGTAAGCAGGACCATGGCTTCTGGTGTAC
GAACCTATATGACCCATACCAATTGGGAGGACACCATCTGGTGCACAAATAATGGAGTC
CATGACCGTGCATGTGATGGTGGATGGGGTGTGAGGCTGGAGCAGGAAATATGGAG
AGACAAACATTGGTACGGGAAACTCGGGTCAAACATTGGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGGTCAACAGCAGTGACTCAAGGGCTGTTGAAGGCCAACATTG
GGGCAAAACATCTTACCGTGGATGATGGTCTGGGGCTCTGGAAATTGATAACCTTGTGAGTG
GTGGTTTCCCTCTGGGCAATTCTGGGCAATATCTCAAGCTCTCTGGGCCCCACATT
ACTCCAAAACATTCCAATTGGCTCAGTTGGGACACATTCTATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACCTGGGCCGTTACTGGACAAAGCAGGGCC
ACAAACAGACCTCTACGTGCCAAGATTCTGCTGTTCTAGGGGAGGCCCTCAACAAAATT
CATTGCTGAACTAGAAGATGTACCTCTGCCAGGCCAAGTCATTCTGGGATGATACACT
CTCAATAGCACTAGTACTTGTGACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCCTCTGAAACCAATGGGAGTTAAGTGGGCACTTGAAAGGTAGGCGGGCATGGCTCATGC
CTGTAATCCCAAGCATTGGGAGGCTGAGAGGGGGATACCTGAGGTGAGGACTTCAAGA
CCAGCCTGGCCAACATGGTAAACCCCGTCTCCACTAAAATACAAAATTAGCCGGGTG
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCAACTGCACTCCAGCTGGCTGACAGTGA
GACACTCCATCTAAAAAA

FIGURE 66

MAPKKLSCRSLLLPLSLTLLPQADTRSFFVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWGLNAIQFYVPWNHYEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFFLAADVSDWFVKLLPKIYWPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQGQNHSRVSASVTKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFLARDVISKFQEVPLGPLPPSPKMMI
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFPEPTPFWVPN
NGVHDRAYVMVDFGVFQGVVERNMNRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKKWWFPLQLPKWPQAPSGPTFYSKTFPILGSGVDTFLYL
PGWTKGQVWINGFNLGRYWTKQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAAACACGCTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTACACTCTCTGGTTATTAGGATACCTTGAGGAATT
CTTTCGAAAAGTCAGAGAAGAGAGCAGTTAGTGCACATTCAGATGTCAAAACGATTT
GCGTTCCTCTTACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGT
CTTGTCAAGAAGTTAGTGAAGAAACTTAGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTACACGCAACGCCAGGACAAGCAGGAGTGCATCTGTCTG
CTGTCGGGGGTGCGCGATGCTGCTTGCACAGACCTGGATGTGCTAAAGCTTGAACCT
AATTCCAGAAGCTAAAATTCTGCTAAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA
TGCTTCACTGAGGTTCACTGATGTGCTGAAATTCTGCCTGGGTGATTGCTAAAAAA
CCTTCGAGAGGTTGACTTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AACTCTCCGAGAGGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGCTCCACATCTACAAAGTTAGTCAATTGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAGAACATCCACATGCTATTTCAGCCTCTCTAATTACAGGAACGGAT
TTAAAGTCCAATAAACATTGCGACAATTGAGGAAATCATCAGTTCCAGCATTAAAAGCAGT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA
AAAACCTGGAGTCACTTATTCTCTAACACAAGCTGAATCCTTACAGTGGCAGTATT
AGTTTACAGAAAACCTCAGATGCTTAGATGTGAGCTACAACAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCAATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACCTCCAGAGAAAGTTGGTCAGCTCTCCAGCTCAGCTGGAGCTGAAGGGGAACCTG
CTTGGACCGCTGCCAGCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAGATCACCTTTTGATACCTGCCACTCGAAGTCAAGAGGCAATTGAATCAAGACATA
AATATTCCCTTIGCAAATGGGATTAAACTAAGATAATATATGCACAGTGATGTGAGGAAC
AACTTCCCTAGATTGCAAGTGCCTCACGTACAAGTTTACAGATAATGCAATTAGGAGTAG
ATACATCTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGAGGTTAAAGTCATTCAATTCCAATCATTTTTTTCTTTGGGG
AAAGGGAGGAAAATTATAACTAAATTGCTTCAAGTCAAGGCTGCTAAAGTAAATGATTAAATTGACATT
GCTGCCGCTACTGAATGTTACAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWILFRIPLKEYSEFKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMICLSELRHLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTLKLVLNLKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS
NNIRTIEEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQOLFCKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQOLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCGGGCTTCTCTGGACTTGCATTCCTTTCATGGACAAACTGACTTTTTTATTCT
TTTTTCCATCTGGCCACCTGGATCCAGGGCGCTGGAAAGACATTGTGTTTACACACATAAGGAT
CTGCTGTTGGGGTTTCTCTCTCCCTGGACATTGGCATTTGCTTGTGGTTGGGGAGGAGCACAGCTGG
GCTCAGTGCTGCTGCACTATCTGCTCTGGTAGTACATCGAAGTCCTTGTACCTCCATACAGTGTATGGCTGTC
ATCCTGCTGGTATCTCTGGCGCTTGTCTCTGGTAGTATGTCTGCTCTGTCTTACTTAAACACAAAC
GGCTAAAGCTGCAAGGAACCTGAAAGCTGTGGCTTGGGCTTAAAGGATACACAAACCCAGACAAAGGTGTTGGGGCCAAG
AACAGCAGGCCCCAACCATGCCCCAGGACTTGTCTGCTGGCTGGAGGTGAGGATATAGAATGTGTGCC
AGTTTGATTCCTGGCACCCTTGTGTTGGGACATAAAATGAGGGCTCCAGGTTAGGAAAGGCTCCCTCTCAAA
GCAGAGGCCCTGAAAGACTCAATGATGTCATGGCCACCTTGTGTGTGAGGCAAGAGAACGGCACAG
CTCCCCATCAGTTCATGGAAAATACTCAGTGCCTGCTGGGAAACAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGGCAACCCCTTGGAGGAGAGAGAACCTCTAGTGGGAAATGCTGATAAACACAGTCA
CACAGCTGCTCTATTCTCACAAACATCACCCTCTGGCTGGGACACTGACCTTCTCTGGAGGTGTCGAAA
GCTGATGTAACACAGGCTTAAAGGCTGTGGCTTAAAGGCTCTGGGCGCTTGGGAAAATGGAGCTTGT
AGAAGGCTCATGCCATGACCTCTTAACTTCTCTCTGGGAGGCTGACAAATGGGGAGGCTGAAAGGAT
GCAAGCTGCAGCTCAGTAGGGGTGCAATATGGCAGAGACCCAAAGGCTGACAAAGGCTGACATCTGCAACTCAATCCC
AGTGAGAACCTGGGACATAAGGAAAGCAGGAAACAAAGGATCAGAAATTATCTTCTCTATGTCAGCTT
GATCCAGATGGAAACTGTGAAAGTAAACATTAAGGCTTGTGAACTCATCAGTACATTGACGTTTCAAATAGTTACT
CAAGTCTGAGTAAACAGGACTATTTCTCTGTATTCTGATTTCTCTCTCTCTCTCTCTCTCTCTCT
GACTCGAGAAAGTAAACAGGACTGTCT
GGCGGTTACCTGGATACCTGGAGGATCTCACAGCCCCAATTACCAAAGGCCGATCTGAGCTGGCTTAT
TGTGTGTTGGCACATCACAGTGGAGAAGTACAGATAAAACTCTTAAAGAGATTCTTCTGAAAGAATAGAC
AAACAGGAAATTGATTTCTCTGGCATCTATGATGGCCCTCCACCAACTCTGGCTGATGGACAAGTCTGT
GGCGGTGTGACTCCACCTGGCATCTGTCATACCTGGGAAACTCTCTGACTCTGTGTTGCTACAGATTATGCCAACTCT
TACCGGGGATTCTCTCTTCTCACCTCAATTATGCGAAAACATCACACTCATCTTCTCTCTCTCT
GACAGGATGAGAGTTTATAAGGAAATCCACCTGAGGGCTTTAACTCTATGGGAAATACTGCAACTAAAA
GACCCAACTTGGCAGGAAATTATCACCAATATACTCACCTTCTGTCATCTCAACTCTGAGTGATCACC
AAGGTAGAAGATCAGTCAAATTACTTCACCAATAATACTCACCTTCTGTCATCTCAACTCTGAGTGATCACC
CGTCAGAAACAAACTCCAGATTATTGTGAGGTGAAATGGGACATAATTCTCACTGAGGATAATACTCACAAACA
GAAGATGATGTAATCAAAAGTCACTGGGAAATATAACACAGCATGGCTTCTTGAATCTCA
TTGAAAAGACTATCTGAACTCACCATATTATGIGGATTGAAACCAACTCTTGTGTCAGTTGAC
ACCTCGATCCAATTGGGTGTTCTGATACCTGTAGAGCCCTCTCCACCTCTGACTTGCACATCTCAACC
TAGGACCTAATCAAGAGTGGATGTAGTGAGATGAAACTGTAAAGGTGATCTCTTATTGGACACTATGGGAGA
TTCCAGTTAAATGCTTTAAATCTGAGAAGTATGAGCTCTGTGATCTGAGTAAAGTTGATATGTGAT
AGCAGTGACCCAGGTCTGCTGCAATCAAGGTTGTCTGGACAGAACAAGGACATCTCTCTCATATAATGG
AAACAGATTCCCATAGGACCCATTCTGCTGAAAGGAGTGAAGTGCAGACTGGCAATTGAGATTCA
GAACACATCGGGAGAAAACCTCAAAACAGGCTTCAACAGTGTGCACTGTTCTCATGGTTCTAGCTCTG
AATGTGTTGACTGTAGGACAACTCACTGAGGGCTTGTGAAATCAACGGGAGACTACAAATACCAGAAGCTG
CAGAACTATTAACTAACAGGTCACCTAAAGTGGAGACATGTTCTCAGGATGCAAAGGAAATGCTACCTCGT
GGCTACACATATTGAAATAGGAAAGGGCTGAAAGTGCACACAGGCTGATGTTAAAAAA

FIGURE 70

MELVRRLLMPLTLLLISCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
EREPENKSIRIIIFSVVQLDPDGCESENKIVFDGTSSNGPPLLGVCSKNDYVPVFESSSSLT
FQIVTDSARIQRTVVFVYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYABININTTSITCSSDRMRVIIISKSYLEAFNSNGNNLQLKDPCTRP
KLSNVVEFSVPLNGCGTIRKVEDQSIYTNTIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSONALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LUVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSVYL
QCKVLIICDSSDHQSRCNCQGCVRSKRDIISSYKWKTDIISGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTATITVRFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAAGAACAGCGCTCCCGAGGCCGCGGAGCCTGAGAGAGGAACGCCGCTCGCCG
GGCAC**ATG**CGCCGCCAGGAGCTCCCGAGCTCGCTTCCGGTCTGCTGTTCTGTTGCTG
TGCTGCCGCCGCCGCCGCGCTGCCAGGCCAGCGCTGCCAGGCCAGCTGCCAGGCCAG
CTGGACGCCGCCAGCTGCCCGCTGGTTGACAGGCCAGCTGCCAGCTGCCAGGCCAG
GGGAGTGTCTTCGTCGCCAGCTTCGGTAGCGAGTGGTTCTGGTGTATTGGCAAAGGAAA
AGATACCGGAAGTATGGAAATTATGGAAAGATAATTACCTCCCTAGTTTCAAATATGAAGAT
TTGGGACCATATTACAGCAAATTATTTTAAATGCCAACAGCTGGGAGCATATTTCAGGG
CTCTGGTCCAAATACATGGCTTAACCTCCAAACATCATGAAGGCTTACCTGGGGGGT
CAGAATATTCTGTGAACTGGAATGCCATAGATGAGGGGCCAACAGGGACATTGTCAAGGAA
CTTGGGTTAGGAACTTCTGGGAAACAGACTGACCTCGCTTTGGACTGTACTATTCCCTTTG
ATGGTTCTACCGCTCTTCTGGGAGATGAATCCAGTGTCTTCTGATGCCGCAATTTCAGG
TTTCTAAGACATTGCCAGAGCTATGAGTTAGTGAACAACATATCAGCTGAGGTTCTG
TGAGCTGATGCCAGGAGGAGCACCGGATCAATCTGGAACAGCACAGGCTTCTGGCTGGT
ATATAATGAAGGCCAGTCTGGGGCACAGTAGTCACCATGATCTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGCTCTATACCTGCACTGATCTGGCTTACATCCAGGACATCTTGG
CATAAATACTGAAACACTGCAATGACAACACTGCTCTGGGGCTATAGGAGGGAACTGG
AATCTCTGATCTATCTTCAATTGAGAATTGGTGAAGCAACTTGTAGAGCACAGTTCTG
GAGGAAACATTCTTGATGAATTGGGCCAACACTAGATGCCACATTCTGTAGTTTGTAG
GAGCGACTGAGGCAAGTGGGCTCTGGCTAAAGTCATGACCTGGCTTACATCCAGGCTTAAG
TACCTGGGCAATCCAGAATGACACTGTCACCCAGATGTTGCTACATCCAGGCTTAAG
AAAAAAATTAGTCATGCCATTCTTCTTAAATGCCCACTCAGGAGCACGCTGCTTCTGG
CCCAAAGCTATTCTGGGGCAACAGAGGGAAACTACTGGGCTATGGACAGCCACTTAAC
GATTCTTGGGCAAAATGCCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC
CGTGAATATTGGGCTGGGCTGGCTCTAGGCCCTAACTAATGCTGAT**CTAAAG**TGCGAGCAG
ATGCTGCAAGTTATGCTAAGGCTAACTGAGCTTACATGGTCTCATTAATTGAGCATGG
AAGCAATGTAACACTGGATAAGAAAATTATTTGGCAGTCAGGCCCTTCCCTTTCCACTA
AATTATTTCTTAAATTACCATGCTAACCAATTAACTCCAGTCAGCTGGCATTAAAGTC
CTTCACATTGATTGTTCTCATGTTGACTCAGAGGTGAGAAATTTCACATTATAGTG
CAAGGAATTGGTGGTATTATGGACCGAATCTGAAAATTATGTTGAGGCAATTCCCGCAT
ATTATATAGTATGACATCACTTAATATGGGATATTCTGGAAATGCTTGTAGCTAAT
TTTTTTGGCCAAACATCATAGAGTGTATTACAAATCTAGATGGCATAGCCTACTACA
CACCATACTGGTATGTTGACTGCTGCCAGCTACAGACATATACTGAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTTGATATGAAACATATGGAAACATAGAGA
GTACAGTAAATAACTGTTAAATAATGGTGCACCTGCTATAGGGCACCTACCCAGAACATGGAG
CTTACAGGACTGGAAAGTGTCTGGGTGAGTCAGTGAAGTGAAGGCCCTAGGGACATT
TTGAACACTGCCCCAGACGTATAAAACTGAGTGTCTTGGCTACACTACATTATAAA
GTTTTCTTCTCAATTATAAACTAACATAAGTGTACTGAACTTTACAAACGTTTAAATT
TTTAAACCTTTGGCTTTGTAAACACTTAGCTTAAACATAACTGCTTAAACATATACT
ATGTAAC

FIGURE 72

MRPQELPRLAFLPLLLLLLPLPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVSPSGSEFWWYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKKFNNANQWADIFQAS
GAKYIVLTSKHHGFTLWGSEYSWNNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLHQVGSWLKVNGEAIYETY
WRSQNNDTVTPDVWYTSPKKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCGGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACCTCCATCGGAGACTAGTTATTGAGCATCTGCCTCTCATATCACCGATGGGCCATC
TGAGGTGTTCCCTGGCTCTGGACACAGGGCTCTGGTCAAGGCTTGGTGCAGAAAGAGCT
CTTCTCACTCCATCTGGACACAGGGCTCTGGTCAAGGCTTGGTGCAGAAAGAGCT
TTCCATCCAGGTGTATGCAGAAATTATGGGATCACCTTGTAGCAGCAAAAGGGCGAACAGC
AGCTGAATTTCACAGAAAGCTAAGGGCCTGTAGGCTGCTGGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAGCTAGGTTGAAACTTGCAGCTATGGCTGGGTTGGAGA
TGGATTCTGTGGTCACTCTAGGATTAGCCAAACCCAAAGTGTGGGAAATGGGGTGGGTG
TCCCTGATTGGAAAGGTTCCAGTGGCCAGTTGCAGCTTCAACTCATCTGAT
ACTTGGACTAACTCTGTCATTCAGAAATTATCACCACAAAGATCCCATACTAACACTCA
AACTGCAACACAAACAGAAATTATGTCACTGAGTACACTCGTGGCATCCCC
ACTCTACAATACCTGCCCTACTACTACTCTCTCTGCCTCAGCTCCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTCACAGAAAGTTTTGAAACTAGCACCATTGTCTACAGAAAC
TGAACCATTTGGTCAAATAAGCAGCATTCAAGAATGAAGCTGCTGGTTGGAGGTGTC
CCACGGCTCTGCTAGTGTGCTCTCTCTGGTGTGCAGTGGCTTGGATTTC
TATGTGAAAAGGTATGTGAGGCCCTCCCTTTACAAACAGAATCAGCAGAAGGAATGAT
CGAACACAAAGTAGTAAAGGAGGAGAACGGCCATGATGCAACCCATAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAACACTACCGTGCATGCTGGAA
GCTGAAGTTT**AGATGAGACAGAAATGAGGAGACACACTGAGGCTGGTTCTTCATGCTCC**
TTACCTGCCCTGGGGAAATCAAAGGGCCAAGAACCAAAGAACAGGATCCACCC
GGTCTCTAAGGAACTAGCTCAGGACTGCCATTGGACTATGGAGTGCACAAAGAGAATGC
CCTTCTCCTTATTGTAACCTGTCGGATCTTATCCTCTACCTCCAAGCTTCCACGCC
TTCTAGCTGGCTATGCTCTAAATCTCCATGGGAGAAAGGAGTTTGCACAAAGTGCAA
GGCTCAAACATCTCATGCTATCCAGTGGTAAAGGGCCTCTGGCTGCTGAGGTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGTTCTCTACTGATCCGAGCTCAGAC
CCTTCTCAGCTTCAAGGAGAACACGTATCCACCTGACATGCTCTTGAGCCCCGTA
AGACCAAAGAGATGGCGAAAAGTTAGCCCCGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTGTAAAGCTAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACT
GTCAAGCAGGACTGTAAACACAGACAGGGCTAAAGTGTGTTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACTTACTTTCTGGCTCTACCTACTGCTGATATTCTCT
AGGAATATACTTTACAAGTAAACAAAATCTTATAAAATTCTTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATCA
ACAACATTTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGAAT
TGAATTATTCTCTAAATAATTGCAACATAGTAAAGCTATCTGGAGACTATTTCTCA
GTTTGATATTCTAGCTTACTCTCAAACCTAAATTCTTATTTCTGGTCAAGCTATCTT
ATTCTTCTCTAATATGGCAACCTTAAACCTTAATTATTAAACATACCTAAGAG
TACATTGTTACCTCTATAACCAAAAGCATACTTAAAGTGCCTTAAACAAATGTATCA
GCCCTCTTCTTCAACAGAAGGGACTGAGAGATGCCAGAAATTGTGACAAAAAATAA
AGCATTAGAAAACCTT

FIGURE 74

MARCFSLVLLTSIWTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNNPKCGKNGVGVLIWKVPVSRQF
AAYCYNNSDTWTNSCIPEIITTKDPIFNTQATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF
GAAAGLGF CYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTGTATTGGTCCCGGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCCTACTCGTGAGGAA
ACTGCGCCGCTCTGCCACGGCTGCCACCCAACCGGAAGACGGTAACCGGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCTGATGTTCTCAGTGCCTTGTGATGATGAAGAACCCAGA
TCCATCACTGTGGAGAACATATAGCAACATTTCTATGGCTACTTACATCACACTCTGCATAGTGTCC
TCTTTCTCCGCTTGGATATTGATGGGCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATGGGCTGTGACTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACAGAACGGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCCAA
TTGGCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
GTACAGGGCTAAATTGGAGGTGGATGGACGCTACTGATGTTAGTACGGGTAC
AAAGTGAGCACATCACCCTCACCAAGCACTCCCTACCTGATCCTGTTCCAAGGGTGC
GGAGGCAATCCGGCGGCCACAGATTGACAAGAACGGACGGCTGTCTCATGGACCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGGGGCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACACAGTGT
GGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTCCTCTGTCAATT
CCAGGCTCTTCCATAACCAAGCCTGAGGCTGCAGCCTTNTNATGTTCCCTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTCTGATTTAAAGAGGCATCTAGGGATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGGCCAAGTGTTCACTGGAGCAAGAAAGAGTC
TCATAGGACGGAGGGGAAATGGTTCCCTCAAGCCTGGTCAGTGTGTTAAGTGT
AGCTATTCAAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTCTTAG
TTGACCTGCACAGCTGGTAGACCTAGATTTAACCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAATTTCCTTCAAGGACTCTGGCTTCTTAAGCCCTTCTGGCTTCTGGTC
TTCATTAAAAGTATAAGCCTAACCTTGTGCGTAGTCCTAACGGAGAACCTTTAAC
ACAAAGTTTTATCATTGAAGACAATATTGAACACCCCTATTGGTGGGGATTGAGAAGGGT
GAA TAGAGGCTTGAGACTTCCCTTGTGTTAGGACTGGAGGAGAACCTGGACTT
TAACCCCTGACATACTCCCCAACCCAGTTGATGGCTTCCGTAATAAAAGATTGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSPVRLSRWLAQPYYLLSALLSAAFLLVRKLPPLCCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFMSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDQSFAPYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTAGCCGTCGAGGAGCTGCCCTGGGACGTTGCCCTG
GGGCCCCAGCCTGGCCGGGTACCCCTGGCATGAGGAGAATGGGCTGTTGCTCTGGTCCCA
TTGCTCTGCTGCCGGCTCTACGGACTGCCCTCTACAAACGGCTCTACTACTCCAACAG
CGCCAACGACAGAACCTAGGCAACGGTATGGCAAAGACCTCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCGCGCGTGTGCGTGTCAAATGGTGGAAAGCT
GTCCGAGAACGGGGCCCCAGAGAAGGAGCTGCTGGTGGCATCGGCTGAGGCACCGCTCT
TTGGGACTACCAAGGCCGCGTCACCTGGCGAGGACAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCCGGGTGTGGTCTTTCTTACAGTCCCCA
ACGGGCCCTACCACTTCAACTTCCACGAGGCCAGAGGTCTGTGAGAGCAGGCTGCCGTG
GTGGCCTCTTGTAGCAGCTTCCGGGCTGGGAGGAGGGCCTGGACTGGTGCAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGCAGCCCTGCCGTGGCC
CAGGCCCTGGCACCTGGCGTGCAGAGCTACGCCCGCCACCGCCGCTGCACCGCTATGAT
GTATTCTGCTTGCCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAACCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTTTGCCCTGGAGTCCATGCCCTGGACCGCTGCAGCCTGGCTGGCTGGAGAT
GGCAGCGTCCGCTACCCCTGTGGTTCACCGCATCTTAACTGTGGCCCCAGAGCCTGGG
CCGAAGCTTGGCTCCCGACCCGAGAGCGCTGTGACGGTGTAACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCTGCCGATCTCCCTACTGGCTGTGATTTATTGAGTGGTT
CGTTTCCCTGTGGGTTGGAGCCATTTAACTGTTTATACTCTCAATTAAATTCT
TTAACATTTTTACTATTTTGTAAAGCAAACAGAACCCATGCCCTCCCTTGCTCTG
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGCATTGCGGTTTGTGGCTCTG
GAGGGTTCCCGCCATCAGGCTGGTCTCCCTCTTAAGGGAGTTGGGCCAGAGTGGC
GGTGGCCTGCTAGAATGCCGCCGGAGTCGGGATGGTGGCACAGTCTCCCTGCCCT
CAGCCTGGGGAGAACAGAGGCCCTGGGGCTCCGGAGCTGGCTTGGCCTCTCTGCC
CACCTCTACTCTCTGTGAAGGCCGTCACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCAGAACATCTGAGGGAGGAAGAACCTCCCTCCCCGTTCCCT
TCCCTCTGGTCTCAAAGAACATCTGTTGTGCAATTGTTCTCCTGTTCCCTGTGTTGG
GGAGGGGCCCTCAGGTGTGTAATTGGACAATAATGGTGTATGACTGCCCTCCGCAA
AA
AA

FIGURE 78

MGLLLVPLLLLPGSGLPFYNGFYYNSANDQNLGNGHKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAAPEKDVLVAIGLRRHRSFGDYQGRVHLRQD
KEHDV8LEIQLDLRLEDYGRYRCVEIDGLEDESGLVELELRGVVFYQSPNGRQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWCNAGWLQDATVQYPIMLPRQPCCGGPLAPGVRSYGRP
HRLRHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHLDR
CDAGWLADGSVRYPVVHHPNCGPPEPGVRSFGFPDPOSRLYGVYCYROH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313.

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FIGURE 79

FIGURE 80

MMWRSPVLLLLLRLHGAQGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPPEESQARLGRIVDRMDRAGDGDGVSLAELRAWIAHTQQRHIRDVSAAWDT
YDTDRDGRVGWEELRNATYGHYAPGEEFHVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFFPHMRDIVAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRSLKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCAC TCGGGCGCAGCCGGGTGGAGCTCGAGCAGGTGGAGCCCCGG
GGGGCGGGCGGGTGCAGGGGATCCCTGAGCCTCTGCCCCCTTGTGCGGGGGTGACACCGATCTG
CCTGTCCTGCTGCTTGGCGCCCGCCTCCCGGGGTGCGGGGGTGACACCGATCTG
GGCTCGCTGCTGATTTGCCCGAGGGCGCTCCAGACCTAGAGGGGCGTGGCCTGGAGCAG
CGGGTCTGCTGCTCTCTCTCTCTGCGCCGGGGGGATCGGAAGGGTGCAGGGGCTCT
GAGGAGGTGACCGCGGGGCTCCCGCACCTGGCTTGGCGCATTCCTCTCTCCAG
GTGTGAGCAGCTATCAGTCAACCATGTCCGAGCCTGGATCCCGGCTCTGGCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGGCCGGAGCGAGGGAGCCGCTCCATTGCTATCACATG
TTTACAGAGGGCTTGACATCAGGAAAGAGAGCAGATGTCCTCTGCCAGGGGCTGCC
CTCTGAGGAAATTCTCTGTGTATGGAAACATAGTATGCTCTGTATCGAGCATATGTGG
GCTGCTGCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTAGCTACC
TGGTGGAGAAAACATTCTCTAGTGGATCCAGTGGCATCCAGTCTCAAATGCTTTCTAGAT
GGTCTGCTTCTTACAGTAATAAGGCAAAAGTAGTACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAACAGCAATAAGAAAACACCGAGAAGAAAATGG
CAATAAAAGATTGTAAGCAGCATTCTGATTGATGGAGCTTAATATTGGCAGC
GCCGATTAAATTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGAAATTGGAAACA
GAAGGACCCACATGTGGCTTCTTCAGGCCACTGAACTGGTCTTCAAGGAACTTCCAAAATAGAATTTCAGTGGAA
AAACTTTACATCAGCAAAGATTTGTTGCCCATAAGGAAGTAGGTTTAGAGGGGTA
ATTCCAATACAGGAAAGCCAAAGCAGTCTGCTCAGGAAATTCTTACCGTAGATGCTGGA
GTAAGAAAAGGGATCCCAAAGTGGTGTGGTATTATTGATGGTTGCCCTTGTGACAT
CGAGGAAGCAGGATTGTGGCCAGAGAGTTGGTGTCAATGTTATGTTCTGGCCA
AGCCTATCCCTGAAGACTGGGATGGTCAAGGATGTCACATTGTCAGAAGGCTGCTGT
CGGAATAATGGCTTCTCTTACACATGCCAACACTGGTTGGCACACAAAATACGTTAAA
GCCCTGGTACAGAACGCTGCACTCATGAAACAAATGATGGTCAACAGACCTGTTATAACT
CAGTGAACATTGCCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCTC
ATGCTGTAATTGTTGAAATCAGGAAACTGGCAGTGGGACATTGGTGCAGGAAAGAT
AGCTGCTGTAAGTTTACTTATGATGCAAGGCACTGGGACTTCAGTTCACTGACTATAGCACC
AAAGAGAATGTCAGTGTCACTGAGAAACATCCGCTATATGAGTGTGGAAACGCTACTGGT
GATGCCATTCTTCTTCACTGTTAGAAATGTTGGCCCTATAAGGGAGAGCCCAACAAAGAA
CTTCTAGTAAATTGTCAGAGTGGCAGTCTTATGATGATGTCAGGCAAGGGCCCTGCACTGCTG
CACATGATGCAAGGAACTCACTATCTCTGTTGGTGTGGCTTGGGACCTCTGGATGACCTG
AAAGATATGGCTCTAAACCGAAGGAGTCTACGCTTCTTACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCACTTGTAGAGATTCTTAGAAATCCAGCAAT
AATGGTAACATTGGACAACTGAAAGAAAAGTACAAGGGATCCAGTGTAAATTGTATT
CTCATATACTGAAATGCTTCTGCACTAGAATCAGATAACAAAATATTAAAGTATGTCAC
AGCCATTAGGCAAAATAAGCACTCCCTTAAAGCCGCTGCCCTCTGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCAATCATGGCTTCTAGAAAACCTAGGAAAGAGGA
GATAATGTTGGATTTAAACCTTAAGAGTTCAACCATGCTTACAATGTCAGGAAAGAGGA
TTCCATAGCTCAATAAAAGAATCTGATACCTAGACCAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSSTQEATGQAVSTAHPPTGKRLKKTPPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHGVGLVQASEHPKIEFYLKNFTSAKDVLFIAKEVGFRGGNSNTGKAL
KHTAQKFFTVDAVGVRKGIPKVVVVFDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSTCYNSVNIAFLI
DGSSSVGDSNFRMLMELFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLA
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

FIGURE 84

MQRIGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLNLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQRMQLCTRSECCG
DQLCVWGHTKMATRGSNGTICDNQRDCQFGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPGASGLLQPHSHSLVYVCKPTFVGSRDQDGEIILPREVPDEYEV
GSFMEEVVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGGAGCTGGGGAAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCCATCCACTCTCTTCCCTCCAAAACACACATGTCATGACACACACATACA
CACACATACACCT
TAAGGCTTAAAGGACAGGCTGGCATTACCTCTCTGAGCTTCCTTGGCTTGTGAGTCAGGTCATAGAAAAGGACAC
CCAGGCTGGTACGTCACACCTGTAATCCACCTGCTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTAGGAG
TTGGAGACCCCTGGCCAACATGGAGAAACCCCATCTCTACTAAATAAAATAAAATAAAATAAAATAAAATAAA
AGGTGCTGTAACTCCAGCTACTCGAGTGGCTGAGCCAGGAAATCTCTGTAATCCAGGAGGCTTCAGGAGGATGGCAGT
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGTGTGACAGAATGAGACTCTGTCAGGAGGCTTCAGGAGGCTTCAGG
GGGGTAGATACTGCTCTCTGCAACCTCTTACTCTGTCATCTCTCTGAGGGCTGCCCCCTGATGGGGCTG
GCAATGACTGAGCAGGCCAGCCCCAGGGACAAGGAAGAGAAGGCATATTGAGGGGGCAAGAAGTGCACGCCG
GTGAGATGACTGCTCTGGGAGGGTGGCTTGGCCCTGCGCAGGCTGACCCCTTACCCCTGCAAAACACA
AAGAGCAGGACTTCAGACTCTCTGTAATGTCAGTGTCCCCCTGCCCTGAGCCTCACCATAGAGGCTTCTGCCCC
ACTCTTCTGACTGCTGGGCTGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
GTGCTGCTGGAGATCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
CTTATTCTGACGCCAGTCCGGCCACTCCCCGAGGACACAGACCTGCTCTGAGAGAACAGACATTTG
CCGGTGGGACAGGAGTGGAGCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
TGCCGAGACTGTGATTTCAGTGCCTTCCCAGCTGCTGAGCCCTGAGAGAACAGCTGACCCGGCT
GGAGGACAGGACTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
CCCCAGGGCTTCTGGCCCTGAGCAACTCTGCTGGGCTTGCAGCCTCAACTCCACCTCTGAGGGGATTGAC
CCCTGTTTGTGAAATGTCAGGCCAACTTGGAGATACTCATGATTGGGGCAACAAGGTAGATGCCATCTGGACAT
GAACCTGGGCCCCCTGGCCAACCTGGCTGAGGACTCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
CCTGGAGGGCTGCAAAAGGCTGGAGGACTCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
GGACAGGCTGGGCCCCGGCTCAAGTCTGAGACTTCAACAGAACTGGGCTTGGGCTTGGGCTTGGGCTTGGG
CACATGCTGCACTTAAAGGGCTGGGACTGAAACATGGAGGACTCTGCTTCTCATCGACAAGTTGCCCC
GAACCTGGGCCCCGGCTGACAAAGTGGACATCAACAACTAACCAACGGCTGTCCTCATCCACCCCCGGG
CACCTGGGCCCCGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
CTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
CAGGGCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
GGGGCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
TAAGACGGTTAGTGTGGTTGGGCTGGCTCTCCAGGGCAGGGGAGGAAAGCTGGGCTTGGGCTTGGGCTTGGG
GGTGGAGGAGACCCCTTACATCTCTGTCATCTCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
CTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
CACATACCCGGCTTCTTCAAGGCCACGGACTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
GTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
TGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
TGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
GGGGCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
GTGCTGCTCCCTCTGCTCTGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
ACCATGTCATAAAATTCTGAAGCTCAGCTGTTCTCAGCAGTAGAGAAATCACTAGAGACTTCTTACAAA
AGAGAAGCAGTCTGGCCAGATGCCCTGCCAGGAAAGGGAGATGGACCCACTGCTTGGGCTTGGGCTTGGG
CAAGACAGATGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
CCTCTGTCGCATTCAGGAAACATCTCAAGAACAGGGAGGACTTGGCTAGAGGCTCTGCCCTCCCATCT
CTCTCTGCCCCAGGGCTCTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
CTTCTCTGTCAGCTGCTGCTCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG
CTGGGGGGGGCTGCCCCATGGGAGTGCACCCAGGGAGTCAAGGACATTTGGGAGAGGGATGCCAGGAA
CGCCATCTCAGCACCCGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG
ATGTGTACCTCCCCAACCCGATTACTCTTCTCTGTTGAAAAATAAAATAAAATAAAATAAA
AAAA

FIGURE 86

MRLLVAPLLLAWAGATATVPVVPWHVCPCCPQCACQIRPWYTPRSSYREATTVDCNDFLTA
VPPALPAGTQTLQLQNSIVRVDQSELGYLANLTELDLSQNSFSDARCDFHALPQLLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRLSLLAGMNLREISDYALEGLQSLSLSFYDNQ
LARVPRRALEQVPGKFLDLNKNPLQRVCPGDFANMLHLKELGLNNMELVSIDKFALVNLP
ELTKLDITNNPRLSFTHPRAFHLPQMETLMLNNNALSALHQQTVESLIPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVFPREMTHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPPEPEIYWVTPAGLRLTPAHGRYRVRVPEGTLELRRVTAAEAGLYT
CVAQNLVGADETKTVSVVVGRAALQPGRDEGGGLELRLVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRRGQGATALARLPRGTHSYNITRLLQATEYWACLOVAFADAHTOLACVWARTKEATS
CHRALGDRPGLIAILALAVLAAHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLWPNPGRKLPRLPRSSGETLPPQLSNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

FIGURE 88

MRQTI IKVIKFILII CYTVYYVHNIFDVFDC TVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSIDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQIQLNNEWTLDKLRLQRLTKNAQDKLELHLFMLSGIPDVTVDLVELEV
LKLELIPDVТИPPSIAQLTGLKELWLWYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKTLLEELHLTGNLSAENNRIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVLQKLQI
NNEGTKLIVLNSLKKMANLTELLELIRCDLERIPH SIFSLHNLQEI DLKDNNLKTIEIIISFQ
HLHRLTCLKLWYNHIA YIPIQIGNLTNLERLYLNRN KIEKIP TQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPP ELFQCRKLRLALHGN NVLQSLPSRVGE LTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFN TLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTGTGCTGCTGCCGTGCTGGGCTGAACGCAGGAGCTGTATGACT
GGCCCACAGAGGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTTATTATGCCACCAACTCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGGCTCTAGCAGTGGATTGGAAACTTGAGGAAATTGGGC
CCCTTGACAGTGTACTCAAACCAACGGAAAACCACCTGGCTCCAGGCTGCCAGTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCACTGGTTCACTGGGTTCACTGGGACCTTACCTGT
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCTGAAGACCTTCTCAGTTGCCCAAAG
AATTCCAGACAGTTCATTCTACATTTCCTCAGAGTCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTCAAGGAGGGACATCAAGTGCACACTTGCGGGGT
TGCCCTGGGTGATTCTGGATCTCCCTGTTGATTGGTGTCTCCTGGGACCTTACCTGT
ACAGCATGTCCTCTCGAAGACAAAGGCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACCTCTATAACATCTTAACATCAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGGCCACCTAGTTGTCTTGTCAAGC
CACGTGAGACACCTACAACAGAGATGCCCTAACGCCAGCTCATGAATGCCCATCAGAAAGAA
GCTCAAAATTATTCTGGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGGGACGAGTTGCTGGAGGGCAGGATC
AACGTGACGGTGATAATGGACAGCTGGATCTCATCGTAGATACCATGGTCAGGAGGCCTG
GGTGGGAAACTGAAGTGGCCAGAACTGCCTAAATTCACTGAGCTGAAGTGGAAAGGCCCTGT
ACAGTGCACCTAAATCTTGGAAACATCTGCTTTGTCAAGTCTACAAAGAACCTTGTCTTC
TACTGGATTCTGAAAGCTGGTATATGGTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAAATGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGACAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTCTAAACCTAACAGATTGGTAAATTGAT
TTGTTTGATCAAATAAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPPLVMWLQGGPGGSSTGFGNFEIGPLDSLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVSLSGPYLYSMSLLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEIMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWRKLWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMLVLTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCT
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTACAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCA**CT**CGGGCGTTGGCGTGGCA
GGGGAGCCTGCGCTGTGGGATTCCCACGTATGCGGAGTGGAGCTGCTCAGCCACCCTGGG
CACTCACGGCGCGCACTGCTTGAACCTATAGTGACCTTAGTGATCCCTCCGGTGGATG
GTCAGTTGGCCAGCTGACTTCCATGCCATCCCTGGAGCCTGCAGGCCTACTACACCG
TTACTTCGTATCGAATATCTATCTGAGCCTCGCTACCTGGGAATTACCCATGACATTG
CCTTGGTGAAGCTGCTGCACCTGTACACTAAACACATCCAGCCATCTGTCTCCAG
GCCCTCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCCCCCACACCCCTCCAGGAAGTTCAGGTGCCATCATAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGAAGGACATTTGGAGACATG
GTTTGTGCTGGCAACGCCAACGGCGGGAGGATGCCCTGCTTCGGTGACTCAGGTGGACCCCTT
GCCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCCAATCGGCCGGTCTACACCAATATCAGCCACCACTTGAGTGGATCCAGAAG
CTGATGGCCCAAGGTGGCATGCTCCAGCCAGACCCCTCTGCCACTACTCTTTTCCCTCT
TCTCTGGGCTCTCCACTCCTGGGCGGTCTTGAGCCTACCTGAGCCATGCAGGCTGGGC
CACTGCCAAGTCAGGCCCTGGTCTTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLLARAGLRKPEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSSLRSHRALAAHFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLsapVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSVWGVGCRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSPWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACACGGTCCCGGGACCGCGTGGGAAGGGCAGAATGGGACTCCAAGGCTGCCCTCTAGGGCT
CTTGCCCCCAGCTGGTCTCCCTGGGCGCTGGGACCCCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAATGTGGAAAAGACTCTCGGACTGTTGAGGCTGTGAGTCTCACCTT
CTCTCCTCAATACGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGCTGAGGCCATCCC
CACTGACCCCTCACACCGTGCAAAAATGGCTTCTGGCAGCCGGAGGCCAGAAGTGCCTTCT
GTGATCACACAGGACTTCTGACTTCTGCTGAGCATCCGACAAGCAGAGCTGCTCTCCC
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGAAACCCATGTTGAAGGTCCCCAC
ATCCCTACCCAGCTTGGGAGGCTTGGGCCCCCATGTGGACTTTGTGGGGGACTCCACCGT
TTTCCCCCAACATCATCCCTGAGCAACCTCTGACCGCCAGGTGACAGGGACTGTAGGGCT
GCATCTGGGGTAACCCCTCTGATCGTAAGCGATAACAATTGACCTCACAAGACGTGG
GCTCTGGCACCAAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTTCCATGAC
TCAGACCTGGCTCAGTCCATGGCCTTCTGGTGGCAACATTGACATCAGGCATCAGTAGC
CCGTGTGGTGGAACACAGGGCGGGGGCGGCCGGATTGAGGCCAGTCTAGATGTGCACT
ACCTGATGAGTGTGGTGGCCAACATCTCCACCTGGCTACAGTAGCCCTGGCCGGATGAG
GGACAGGACCCCTTCGACCTGGCTCATGGCTCTAGTAATGAGTCAGGCCCTGCCACATGT
GCATACTGTAGAGCTATGGAGATGATGAGGACTCCCTCAGCGCCCTACATCCAGCGGGTCA
ACACTGAGCTCATGAGGCTGCCCTCGGGGCTCTACCCCTGCTCTCGCCCTCAGGTGACAGT
GGGGCGGGTGTGGTCTGTCATGGAAACGACACCAAGCTTCCGCCCCCTACCTTCCCTGCCCTCAG
CCCTATGTCACACAGTGGAGGCAACATCTCCAGGAACCTTCCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCTAGCAATGTGTTCCACGGCTTCTACACAGGAG
GAAGCTGTAACGAAGTCTCTGAGCTCTAGGCCACCCATCCAGTTACTTCATG
CAGTGGCCGTGCTCTGGAGATGTTGCTGCACTTCTGATGGCTACTGGGTGGTCAAGAAC
GAGTGCCTTCCATGGGTGCTGGAAACCTCCGCCCCCTACTCCAGTGTGTTGGGGATCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCTCTGGCTTCTCACCCAAG
GCTCTACAGCAGCATGGGGCAGGGTCTCTGGATGTAACCCGTTGGCTGCCATGAGTCTGTC
TGGATGAAGGGTAGAGGGCAAGGGTTCTGGCTCTGGCTCTGGATCTGTAACAGG
TGGGGAAACCAACTTCCACCTTGTGAAGACTCTACTCAACCCCTGACCTTTCTATC
AGGAGAGATGGCTTGTCCCCCTGCCCCCTGAAGCTGGCAGTTCACTGCTTATTCTGCCCTGTTG
GAAGCTCTGCTGAACCCCTCAACTTGTACTGCTGAGACAGCTTATCTCCAAACCTGAAA
TCTGCTGAGCTTGTACTGACTTCCACCCCTACATCTCATCAACTCAGGTCTCCCTACT
CTCTGCCCTAGATTCTCAATAAGATGCTTAACGATTTTGAATGCTCTCCCTCGC
ATCTCATCTTCTCTTCAATCAGGCTTCTTCCAAGGGTTGTATACAGACTCTGTCACCA
TTTCACTGTATATTCACTTCCCAATTCACTGCAAGGGACACCTCTACTGTACCGTTTACTCT
TTCTACCCCTGACATCCAGAAACAAATGGCTCCAGTGCATACTTCTCATCTTGTGTTTATG
GCCCTTCCATCATGTTGCCACTCCCTCTCTTACTTGAAGCTTCCAGGTCTTAACTTCTG
ACTACTCTGTCTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCAATTG
TCCATTGTAGATTGTCTCTCATGTTACTCATTGTCCCCCTGGAAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATACCTCAA
TGAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSFTALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLAAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGLHRFPPSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSDVGSCTSNNSQACAFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYIISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEVGQGFCSGPGWDPVTGWGTPSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCTCCGGGCCACACCTGTCTGAGCGGCGCAGCGAGCCGGCCGGC
GGGCTGCTCGGGCGGAACAGTGCTCGGCAATGGCAGGGATTCCAGGGCTCTTCTTC
TTCTTCTGCTGTGCTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCACTTG
GCCGTGCAACCGCCTCGTGTGCTTGGCCAGTCTACCCCAATTAGCCAAGCCAGACT
TTGGAGCGAAGCAAATTAGAAGTATCTCTTCATGTGGACCCAGTGTCTATGCAAGGAACT
CCACTGCCCACCTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTATGCCAATGG
CAGCCGACAGAGACGCAAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTGAAGGAAGCGGAGATTTATGGCTATGACAGC
AGGTTCACTGGGAAAGGACTTCTGCTCAACTACCCCTCTCACATCAGTGAAGTT
ATCCACGGCTGCACGGCACCTGGTGGCAGAGAAGCAGTCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCAGTGGCTTCTAAAGCCC
AAAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA
ATTTCACTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCAATGGATTATGATTATGCCCTCTGGAACTCAAAAGCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGGCCCTCTGCTAAGCAGTCCAGGGGCAGAATTCACTTCTC
TGTTTATGACAATGACCGACCAGCAATTGGTGTATGCTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGCAGGCTGGCTAT
GTGAGGATGTGAAAGAGACAGCAGCAGAAGTGGGAGCAGAAAATTATTGGCATTTCAGG
GCACCACTGGGTGGACATGAATGGTCCACAGGATTCAACGTGGCTGTGAGAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATAAGGAAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTCCCTCTGGCAGCAATTAGGGCTTCATGTTCTTATTAGGAGAGCC
AAATTGTTTTGTCTTGTGACACGTGTGTGTGTGTGTGTGTGAAAGGT
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATTGACAATTAAAGTTAATCTCACGTTTG
CAAACTTGATTTTATTCTGAACCTGTTCAAAGATTATTAATTTGGCATA
CAAGAGATATGAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQH
RDSGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTS
VKLSTGCTGTLVAEKHVLTA
AHCIHDGKTYVK
TQKLRVGFLPKFKDGGRRGANDSTS
AMPEQMKFQWIRVKRTHVPKGWI
KGNANDIGMDYDYA
LLELKKPHKRKFMKIGVS
PPAKQLP
GGRIHFS
GYDNDRPGNL
VYRFCDVK
DETYD
LLYQQCD
AQPGASGSGVY
V
Y
V
R
M
W
K
R
Q
Q
Q
K
W
E
R
K
I
I
G
I
F
G
S
H
Q
W
V
D
M
N
G
S
P
Q
D
F
N
V
A
V
R
I
T
P
L
K
Y
A
Q
I
C
Y
W
I
K
G
N
Y
L
D
C
R
E
G

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGTCTCTGAGCTGCTGCCGCTCCCCCCCCACCAGCCATGGTGGTT
CTGGAGC~~GCCCCCAGCCCTGGTGGGGCTGTCGGCACCTCACCTCCCTGCTGCTGCTG
GGCTGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACGGGTTGTCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCAGAAGAATGGGACCCACCAC~~TGCGCAGGTTCTGCTCACCA~~GCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTGCTGCTGCTGG
GGCCTGGCAGCTGGGAAACCTGGCTCTGTCAGAGGTGGTGTGCTGGGTGAGC
CCCACCCCTGTGATTCCCTGAAAGGAAGGTGGCTGTGAGACATTGCCCTGGTGCGTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGTCTGCCCATCTGCCACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTG
CCCACCCCTCAGACCCCTGCAAGAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCGCGCTACTT
GGAGGGGAGCGGATGCTGCTGGC~~GACTCGGGGGCCCCCTCATGTGCCAGGTGGACG~~
GCCCTGGCTGCTGGCCGGCATCATCAGCTGGGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTGCGCACCGCTCC~~TGGGTGAGAAGATCGTCAAGGGTGCA~~
GCTCCCGGGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCC
CCCGCGCTCCTAGGGCGCAGGGAGCGCGGGCTGGATCTGAAAGGGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCCCTGGCGGTTCCCGCTGGTAAATAGGCTCATCTACC
TCTACCTCTGGGGCCGGACGGCTGCTGCCAAAGGAAACCCCTCCCGACCCGCCGAC
GCCCTCAGGCCCCCTCAAGGCATCAGGCCGCCAACGGCTCATGCCCCGCCAC
GACTTCCGGCCCCGCCGGCCAGCGCTTTGTATATAATGTTAATGATTTTAT
AGTATTTGTAACCCCTGCCACATATCTTATTATTCTCCAATTCAATAATTATTATT
CTCCAAAAAA~~

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWRVITAHHCFKDNLNKPYLVFSVLLGAWQLGNPGRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWEKIVQGVQLRGRAQGGGALRAPSGQ
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGGCCACATGCGACGGCTCTGCAAGTTCTGTAGTCTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACACAGGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTGTGGT
GGAGCTGCACAAACCTCTACCGGGCCAGGTATCCCCGACGCCCTCAGACATGTCGACATGA
GATGGGACGAGGAGCTGGCCGCTTCGCAAGGCTTACGACAGGCACTGCGTGTGGGCCAC
AACAGGAGCGCGGGCGCCGGCGAGAATGTTGCGCATCACAGACGAGGGCATGGACGT
GCCGCTGGCATGGAGGAGTGGCACCCAGAGCGTGAGCACTACAAACCTCAGGCCGCCACCT
GCAGGCCAGGCCAGATGTGGCCACTACACGCAAGGTGGTATGGGCAAGACAGAGGAGTC
GGCTGTGGTITCCCACITCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCGGGGAACGTGAAGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCAAATGTCCTCTGGCTACCACTGCAAGAACCTCCCTGTGAACCCATCGAACG
CCGGAAGATGCTCAGGATTGCTTACCTGGTACTGAGGCCCCATCTTCCGGCGACTGA
AGCATCAGACTCTAGAAAATGGTACTCTCTTCTCCCTAGCAACGGGATTCCGGCTTTCT
TGGTAACAGAGGCTCAGGCTCCCTGGCAACCAAGGCTCTGCTGTGGAAACCCAGGCC
CCAACCTCTTAGCAACGAAAGACCCGCCCTCATGGCAACAGAGGCTCCACCTTGGCTAAC
ACTGAGGTTCCCTTCCATTGGCAGCTCACAGCCTGCCCTCTTGGATGAGGAGGCCAGTTA
CTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGAACAGACAAAACA
AAAGTGCCTCTAGGAGGCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGCAAG
GGAACCTCACCCATGCCAGGAGGAGGTGAGGCTGAGGCTGAGTTGCCCTTCCAGTG
AGGTCTGGCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGGCTGAGGCCACACTGGAC
CACAGGGCACACCTCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGTGGCGTGCCTGGCTCTGCACTGCTGTGGCAGGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGGCCCTGGTCATGTGTTGGGCCCTCTCTGGG
CTACTGCTCTGCTCTCTGGTGTGGCTGAATCTCTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTCACTGCTCTCTGTCACTCTCCCCACCCCTGCCCCAGGCCCTAAACAAGATA
CTTCTGGTTAAGGCCCTCGGAAGGAAAGGCTACGGGCATGTGCCCATCACACCATCC
ATCCTGGAGGCCAAGGCCCTGGCTGGCTCGAGCTCAGGAGGCCCTGAGGACTGCAACCC
GGGCCACACCTCTGCCCTCCCTCTGAGTCTGGGGTGGAGGAGTTGAGGGAGCT
CACTGCTCACCTGGCTGGGCCACAGCATGTCGCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC
TTGAGTGGGGAGGCAGGGACAGGGAGGAAAGTAACCTCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLVAATTGPGVGAALTDEEKRLMVELHNLYRAQVSPTASDMILHMRWDEELAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVETNIELLVCNVYEPGPNVGKRPYQEGTPCSQCPSGYHCKNSLCEPIGSPEDAQDLPLVLTAEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEVSGSLATKALPAVETQAPTSLATKDPMSMATEAPPCVTTTEVPSILAHSPLSDEEPVTFPKSTHVPPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAFAEALPPSSEVLASVFPFAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVVSGLNSGPGHVWGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACTGAAAGTCAGGCTTTCAATTGGGAAGCCCCCTAACAGAACTTCGGTCATTCTCAAGATTTGGTGGACGT
ACTTCTGTGTCTCCCTCTGCTTCTTTTACATTAGCAGACGGCTTAATCACAACAGATTATCTCAT
CAAGGCAGGTTCCATGAGCCACCTCAAGCCTCGAGAAGTGAACAAACAACTGAATGGAGACCATTC
AAATCTGGGACCATGCTGCAAATATTACACTTCTCTTGGCTGGAAACAGGATTTGAGAATACTCCCTGA
ACATCTGGGACCATGCTGCAAACCTTGGACCTTAGGACCAAACAAATTTCAAGCTCCAAACTTCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTAACAGCAGGACTCACATCAATGGAACTTGGGTATTTGACAA
TTTGGCCAACACACTCCCTGTGTTAAAGCTGAAAGGGAACTGTCAGCTATCCCAACCCAAAGATGTTAAACT
GCCCAACTGCAACATCTGAATTGAAACCGAACAGATTAAAGATGAGATGAGCTGACATTCAAAGCCCTGG
TGCTCTGAAGCTCTGAAAATGCAAGGATACAGGAAACTTATGGATGGAGCTTITGGGGCTGAGCAA
CATGGAATTTGAGCTGGACCATAACAACTAACAGGATTTACAGGCTGGCTTACGGCTTGATGCT
GCAGGAACATCTGAGCTGGACCATAACAGGATCACCCCTGATGCCCTGGGAGTTCTGGCAGAACGCTCAG
TGAGCTGGACCTAACATCTAACATCAGGTTAGTGTATCAGGTTCTGGCCTAACGTTACTAAATAC
ACTGCAATTGGNAACACAGAGTCAGCTACATTGCTGATTGTCCTTCGGGGCTTTCAGTTAAAGACTT
GGATCTGAAGAACATGAAATTCTGGGATTAGAACAGCTGAAAGACATGAATGCTTCTGGGCTTGACAACACTGAG
GGCAGCTGATACTCCAAGGAAATCTGGATCGCTTATATTAAAAAGCTCAGTGTGATGGAGCA
TCTAGAGCTTCTGAGTGAACAGCAATCTGTTTACAGGCAATGCTTACAAATGAAAGAAACTGCAACAAATT
GCATTAATAAACATCACAGCCTTTGGCGATTCAGGCACTAAAGTGCCTTACAGTGGTGGCGGAAACRAACTT
TCAGAGCTTGTGAAATGCTTGGGAGTGGCTCTGGCTAAAAGGAGAAGCATTITGCTGTTAGCCAGA
TGGCTTGTGTTGATGATTITCCAAACCCAGATCAGGCTCAGGAGCTGATGCTGTTAGCCAGA
CAATTGAGTTCTACCTGCTCAGCTGGCAGGAGCTGATTCCAACTGACTTTGCTTGGAAAAGAACATGA
ACTACTGCACTGATGTAATGGAAATTTACATGCAACCTCCGGGGCAAGGTGGCAGGAGTGGATGACTTACAC
CATTCCTGGCTGGCGAGGTTGGAAATTTGCGCATGGGGAAATATCAGTGTGATCTCCAACTCATTTGGTC
ATCCTACTCTGCTAACAGCAGCTAACAGTAAATATGCTTCCCTCATCACCAGACCCCCATGGATCTC
CCAGCTGGGCAATGGGCTTGGCAGCTGGGAGGAGGAGCCTGATGTTGATGCTTCCACTAAC
TGGGGGCAAGACTTCCCACTGGCAGGAGGAGCCTGATGTTGAGTGGGAGGATGACGTTCTTATCGT
GGATGTAAGAGATAGGAGCATTGGGATACAGCTGACAGCTCAGGAAACTTGGCAATAAAGCAGT
AACTCTGACTGCTCTAGAAACCATATTCTGGGCAACTGTTGGCAGGAAACTGTAACCAAGGGAAACAGC
CGTCTCATGCTGGATCTGGAGGAGGAGGCTCCCTAAACTGAACTGGACCAAAAGATGATGGCCATTGGTGG
AACCGAGAGGACTTTGGCAGGAGCAATCAGTCTGTTGAGTATGGACTCAGATGTCAGTGAATGCTGGAA
ATACACATGTGAGATGCTAACACCTTGGCACTGAGAGGAGAACCTGGCCCTCAGTGTGATCCCCACTAAC
CTGGCAGCTCCCTCAGATGCAAGGACCCATCTTAGAGCATGAGCTGGGCAACTGTGGTGTGCTGATCATGC
CTGGGTTGTGTTGCTGGGGCACTGGTGGGGCTCATCATACACACAGGGAGGAAATGAGA
TTCAGCAGCTTACACAGATGCTGGGAGGAGGAAACTTGGCAGGAGATATCTGAGTATTGTCATCTGGGAA
AGCTGCAAGGGAGGATGGTGTGCTCTGAGAACTGGGACCTGGCCATATTGCAATAGCAGTGAAGCTGATGG
ATTTTCTTACACAAACATGACAGTACTGGGACCTGGCCATATTGCAATAGCAGTGAAGCTGATGG
CACAGATGCTTCTTGGGGCTTGGGGCTTGGGGCAACTGGGCTTGGGGCAAGGGAACTGGGAGG
TCTCTTGGGGAAACATGATCATACAGGTTCTGAGCTGGGGTGTGCTCATATACACACAGGGAGGAA
CATAAAGGAAAAGGAGTGGTACCCCAGTCTCAGCTTCACTCTTCAAGAAGAATCTGGCAACGGAGCT
GTGGCTTACATGAGTGGAGGAGCTAACACACTAGTTACTCTCAGATGAGGAACTGGGAGG
TCTAAACAGTCTCTTGTGAAATGCAATCCAGGGCTCGGTTGGCTCGAGTAATTCTTCT
TACCTGGGGAAAGGCTCAGGAGACCTTCACAGATGCTCTTCAAGGCTTGGGAGGCTCAGATGTCAGCC
AAGAGCTTATTTGAAAGCTTCTTCCCGACAGCTGGACTCTGGGGTCAAGAGGAGATGGGGAAAGAAC
AGATTTTCAAGGAGAAAATCACATTGTTACCTTAAACAGACTTGTAGAAGGAAACTACAGGACTCC
TTATGACTTGGGACACATAGACTGAATGAGACCAAAAGGAAACTTAAACACTACTCT
AAAGAGAGGAAATCTTATGTTTAAATGGAGTTGATGTTAAAGGATAAAAATGCTTATTTACAGAT
GAACCAAAATTACAAAAGTATGAAATTTTACTGGGAATGATGCTCATATAAGAATACCTTTAAACTA
TTTTTAACTTTGTTTATGCAAAAAGTATCTTCACTGAAATTAAATGATATAATCATGATTATTTATGTTT
TTAAATGCGAGATTCTTCTTGTGAAATGACTTAAAGCATTTTAAATAATCTGGCCTTGTACCATTTT
TTAAATGAGTACTTCATTATTTGCACTTATTTAATAAAAGTGTCAATTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRSLFIKASSMSHLQSLREVKLNNELETI PNLGPV SAN
ITLLSLAGNRIVEILP EHLKEFQSLETLDLSNNNISELQTAFPALQLKYL LNSNRVTSMEP
GYFDNLANTLLVLKLN RNRISAIPPKMFKL PQLQHLELN RNKIKNV DGLTFQCLGALKSLKM
QRNGVTKLMDGAFWGLSNMELQLQDHNNLITEITKGWL YGLLMLQELHLSQNA INRISPDAWE
FCQKLSLELDLTFNHL SRLDDSSFLGLSLLNLT L HIGNRVSYIADCAFRGLSSLKTL DLKNN E
ISWTI EDMNGAFSGLDKLRL L LQGNRIRISITKKAFTGLDALEHLL DLSDNAIMSLQGNNAFSQ
MKKLQQLHLNTSSLLCD CQLKWL PQWVAENN FQSFVN AS CAHPQLLKG RSI FAVSPDGFVCD
DFPKPQITVQPE TOSAIKGSMNLSFICSAASSSDSPMTFAWKKDNE LLHDAEMEN YAH LRAQG
GEVMEYTTILRLR LREVA FASEG K YQC V ISNHFGSSY SVKA KLT VNMLP STKTPMDLTIRAGA
MARLECAAVGHPA P QIAWQKDGTDFP AARERRM HVMPEDDVFFIVDV KIEDIGVY S CTAON
SAGSISANATLTV L ETPSFLRPLLDRTVT KGETAVLQCIAGGS PPPKLNWT KDDSP LVVTER
HFAAGNQLLIIVDSDVSDAGKYTCMSNTLGTERGNVRSLVTPPTCDSPOMTAPS LDDDG
WATVCGVIIIAVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPS YLSSQGT LAD
RQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATD LFLCPFLGSTGP
MYLKG NVYGSDFETYHTGCS PDPRTVLMHDYEP SYIKKKEC YCPSH PSEESCERSFSNISW
PSHVRKLLNLSYSHNEGPGMKNLCLNKSSLDF SANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDSGSEEDGKERTDFQEE NHICTFKQTLE NYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459, 628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268, 314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653, 671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962, 1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534, 612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGGTGGCTGCCTTGCAAAATG
AAGGATCAGGACGACGCTTCTCTGGAACCGAACCGCAATGGATAACTGATGTGCAAGAGAGAAGGAAAC
GAAGCTTTCTCTGTGAGCCCTGGCTTAACACAATGTGATATGTGACACACAGGGAGCATTCAAGAATGAAA
TAAACCGAGGTAGACCCGGGGTTGGTGTGCTGACATAATAATCTTAAGCAGCTGTTCCCTCC
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAAGAAGAAAAGATGTGCTATTCTC
TATAAAGGAGAAAGTGGAGCCAAAGGAGATTTTTGGAAATGAAAAGTTGGGCTTTTTAGTAAAGTAAAGAACT
GGTGTGGTGTCTTCTTGTGAATTCCACAAGAGAGGAAATTAATAATCATCTGCAAGAAGAAA
TTTCAGAGAAAGAAGTTGACCGCCGAGATTGAGGCAATTGATTTGGGGAGAGAAACAGCAGACAGTTGGA
TTTGCTCTATGTTGACTAAATTGAGGAAATTGAGGCTTCTCATCAACCTCCCTTTTTAAAT
TTTATTCTTTGGTATCAAGATCATGGCTTCTCTGTGCTTCTAACACCTCGATTCCATCTGGATGTTGCT
GTGATCAGTGTGAATAACAGGAGATTGAGGACCAACACAGATAAAATTATGAATGTTGAACAAAGAT
GACCTTACATCCCACAGAGATACTTGTGATAGGCTTACAGGGCCATTGACCCCTGCTTGTGGTGT
GCTGCTCTCAACTCTGTGCTGGCTGGTCTGGTGCAGGGCTCAGACCTGCCCTCTGTGCTCTGAGCAA
CCAGTCAGGAAGGTGATTGTGTCGGGAAACCTCGCTGAGGGATGGCATCTCCACCAACAGGCT
GCTGAACCTCATGAGACCAAACTTCAAGATCAACAGCTTCAAGACTTGGAGGACTCTGGAAATCT
ACAGTTGAGTAGGAACCATGAGACCAATTGAAATGGGGCTTCAATGTCGGGAAACCTCAACACTCTGG
ACTCTGACAATCTCTTACTACCATCCGGATGGAGCTTGTATACTGCTTAAACATGAGGACTCTGGT
GGCAAAACCCCCATTAGAACGACCTCTTATGGTTAAACAGAATTCTTCTTGGCCGACTGAGCTTGG
GGAATGAAACAGCTTACATCATCTGAGGCTTGTGAGGTTCTGTGAGGTTATTGAAACCTTGC
CATGTGCAACCTCGGAAATCCCTAACCTCACACGGCTCATAAAATAGATGAGCTGGATCTTCTGGAAATCA
TTTATCTGCATCAGGCCATGGCTCTTCTGGGTTGATGACCTTCAAAACTGTGAGTACAGCTCCAGAT
TCAGATGATTGAAAGCATGCTTGTGACACCTTCACTGGATGAGTACACTGGAGATCAACCTGGCACACA
AAATCTAACATTACTGCTCATGACCTCTTCACTCCCTGGCATCATCTGAGCAGGATACATTACATCACA
AACTCCACATGGCTTCACTGGGATGGCATCTGGGATGGCATCTGGGATGGCATCTGGGATGGCAT
TAACACTCCCTCCATCTTAAAGGGAGGTACATTGGAGAGCTGAGGAAATTTACTCATGCTATGCTCGGT
GATITGAGGCCCCCTGAGACCTCAATGTCACTGAGGACATGGAGCTGAGCTGAATGTCGGGCTCCACATC
CCGGACATCTGATCTTGTGATCTTCAACATGGACACTGATGGGGCGTACAAAGTGGGATGGCT
GCTCAGTGATGTAAGTGAATTTCAAAATGTAAGTGTGAGGATGACAGGATGACACATGTTGAGTAA
TTCGGITGGGAATACTCTGCTTCAGCCCTGGATGTTACTGTGAGGACCAACTACTCTTCTCTTAC
AACCGGTACAGTAGAGACTTGGAACCGACCTCTTCACACCAAGGACAGGACAAAGTGGCACAGAGAAA
AGTGGTGGACTGGGAGACCAATGGGACCCACTCTTCACACCAAGGACAGGACAAAGTGGCACAGAGAAA
CACCATCCAGTGAATTAACAGTGGGATCCAGGAATTTGTGAGGCTCATGAGAATCTACCAAAATCTCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTGAGCTGAGCTGCTGCTTACAGAGTGGAGGAAAGCAGC
TCGGAAAACCATCACGCCCAACAGGACTGTTGAATTTAAATGTGGATGATGAGGTTACGGGAGACACCC
CATGGAAAGGCCACCTGGCCATGCCGTATCGAGGATGAGCAGCTAAATCACTATAACTCATACAAATCTCC
CAACACACACACAGTTAACACATAAATTCATACACAGTTGAGCTGAGGTTATTGATCGGAATGAA
CTCTAAAGAACATGTAAGAGACTCAATCTAAACATTTACAGAGTTACAAAAAACAAACATCAAAAAAAA
GACAGTTTAAAGAACATGACCAAAATGACTGGGCTAAATCTACTGTTAAAGTGTCTTACAAAAAA
AAAAAGAAAATTTTATTAAACATTTGTGATCTAAACAGACAAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIVKNSFKHLRHLIELQLSRNHIRTIEIGAFNGLA
NLNTLELFNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDGLGELKRLS
YISEGAFEGLSNLRYLNLMCNLREIPNLTPPLIKLDELDLSGNHLSAIRPGSFQGLMHQKL
WMIQSQIQVIERNAFDNLQLSILVEINLAHNNTLPLLPHDLFTPILHHLERIHLHHNPWNCCDIL
WLSWWIKDMAPSNTACCACRNTPPNLKGRYIGELEDQNYFTCYAPVIVEPPADLNVTGMAAE
LKCRASTSLTSVSVITPNGTVMTGAYKVRIAVLSDTLNFTNVTQDGTGMYTCMVNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFITPVDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDETGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGEQPGSVAERPCPTCRLGLDILDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT
LLSLAGRNRIEVLPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYNSNRVTSMEPGY
FDNLANTLLVLKLNRNRIASAIPIPKMFKLPQLQHLELNRNKIKNVDGGLTQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNNLTFITKGWLYGLLMLQELHLSQNAIRISPAWEFC
QKLSELDLTFNHLRSRLLDSSFLGLSLNNTLHIGNNRVSYIADCAFRLGSSLKTLDLKNEIS
WTIEDMNGAFSGLDKLRLRLLQGNRIRSIKKAFTGLDALEHLDLSDNAIMSLOQNAFSQMK
KLQQLHLNTSSLCDCKLKWLPQWVAENNNFQSFVNACAHQPLLKGRSIFAVSPDGFCVDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNEELLHDAEMENYAHHLRAQGGE
VMBYTTTILRLEVEFASEGKYQCVISNHFGSSYVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPKLNWTKDDSPPLVVTTERHF
FAAGNQLLIVDSDVADGAKYTCMSNTLGERGVRLSIVPTPTCDSPQMTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITMIDETNLPADIPSYLSQGTLLADRO
DGYVSSESGSHHQFVTTSSGAGFFLPQHDSSTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVNYGSDPFTYHTGCSPDPTVLMHDYEPSTIKKKECYPCHSPSEESCRSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSLDPSANPEPASVASSNSFMGTGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDSGSEEDKERTDFQEENHICTFKQTLHENRTPNFQSYLDLT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFAEEEPVLVLSPEEPGPGPAAVSCP RDAC SQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEK IYPEELSRLHRLT LNLQNNRLTSRGLPEKA FEHLTNLYLYLANNK
LT LAPRFLPNALISV DFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGL P DNM FNGSSNV
EV LILSSNF LRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ET FWKLSSLEYLDLSSNNL SRVPA GLP RS L VLLHLEKNAIRS VDANV LTP IRSLEY L LHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLP RVR TLMILHNQITGIGREDPATTYF
LEELNLNSYNRITS PQVHRDAFRKLRLRS L DLSGNRLH TLPPGLPRNVHVLKVKRNEAALA
RGALAGMAQLRELYLTSNRLRSRALG PRAVVDLAHLQ LLDIAGNQLTEI PEGL PESLEYLYL
QNNKISAVPANAFDSTPNLK G IFLRFNKLAVGSVV DSAF RRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGCGCGCGCAGCAGACCTGCTCCGGCGCGCGCTCGCCGCTGCTCTCGGGAGCGGGAG
CAGTAGCCCGGGCGCCGAGGGCTGGGGTTCTCAGGACTCTCAGAGGGGGCTCCCATGGGCCAACACCC
CAACCTGCTTCCCTCGGCTCACCTGCGCCAGGACCCGCTGCCAACATGGGATTTCTCTGGCGCTGGT
GCTGGTATCCCTCGGCTCACCTGCGCCAGGACCCGCTGCCAACATGGGATTTCTCTGGCGCTGGT
TGGCCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTGCCAGTCTGGGGAGCTGTCGACG
TGTGCGGCAACCCAGCTGCAAAACATGGTGAATGTAATGGGCAAAACAACTGCAAGTGTCACTCTGGTTATGCTGG
AAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCGGCCCTGTAAAGCACAGGTGATGAAACACTTA
CGGCGAGCTACAAGTGCTACTGTCGAGTGGCTGTGATGGGAAATATAGCTCATGCCGATGTTCTGCTCAAGTGCCTGACCTG
CTCCATGGCAACACTGCTAGTATGGCTGTGATGGTGTAGATGTGATGTCAGCGAACAGGCTCTGCCCTAGATT
GCACCTGGCTCTGATGGGAGGACTGTTGAGATGTGATGTCAGCGAACAGGCTCTGCCCTAGATT
TAGGCAATGTCGTTCAACACTTGGGAGGCTACATCTGCAAGTGTCAAAAGGCTTCATCTGATCTCATGTTATGGGAG
CAAATATACATGTCGATGACATAGACAGAACATGTCGACTGTGCACTGTCAGTGTGCAAGCAGCTTGTGCTGATGTTATAA
CGTACGTGGGCTTACAAGTCAAAGGATAACAGGGTGAATGGACTGACTTGTGTTATATCCAAA
AGTTATGTTGAAACCTTCAGGTCCTATCATGTCACCTGGGAAAGGAAATGGTACCATTTAAAGGGTGAACAGGAAA
TAATAATTGGGATTCCTGATGTTGGAGACTTGTGGCTCCGGCAAGACACCCATATATCCCTCTATCATTCACCA
CAGGCCACTTCTAACGCAACAAACAGGACTCACCCAAAGGCAACACCAAACTCTAACCCACCCACCCACCC
CTGCCAACAGAGCTGCAAGAACCTCTACCCACCAAGGCAACAGGACTGACAACTATAGC
ACACAGCTGGCAGTACACCTCCAGGGTAACTGACAAAGGGTACAGACAGACCCCTCAGAAACCCAGAGG
AGATGTTGTTGTTGTTGAGTGTGAACTGGTGAACAGTGTGTTGACATGGGAGGAAAGAGACAA
TGACTTGGCACTGGGAACCAATCAGGGACCGAGCAGGGACAAATATCTGACAGTGTGCGCAGCAGGCAAAACCCAGG
GGGAAAGCTGCACTGGCTTCTGGCTCATCTCCGGCCCTCATGCTCATGGGGACCTGTGCTGTGATTCAGGCA
CAAGGTGACGGGGCTGCACTTGGCAACACTCCAGGTTGTTGAGAAAACACGGTGCACAGGAGCAGCCTGTG
GGGAAGGAAATGGGGCTGAGGGAAACACAGATCATCTGGGGCTGACATCAAGAGGCAATCACA
AAAGATGATTAAAGGGTTGGAAAAGGAAATGCTATGTTGAGGAAATGGGATTATTGAGGCTGGAGAAG
AGAAGACTGGGGGCAAAACCATTTGATGGTTTCAAGTATATGAGGGTTGGCACAGAGGGTGGCACAGCAGCTG
TTCTCCATATGCAATGAGAATAGAACAGAGGAAACTGGCTTAGAGTATAAGGGAGCATTTCTGGCAGG
GGCCATTTGTTGAAATACTCTAAAAAAGGAGTGTGAAATCTCAGTATCTCTCTCTTCTAAAGGTTAGA
TAAAAAATTGTCATTAAAGATGGTTAAAGATGGTTTACCCAAAGGAAAGAACAAATATAGAATTTCACCA
AGATGTTTGATCTCTAGTAGTGTGAGTAACTTGGAGGAAACATTTAGAACTAAATATTGGACAAGGCTTAAATTAGG
CATTTCCCTCTGGCACTCTAAATGGAGGGATTGAAAGGGGAGAGGCCAACAAATGCTGAGCTACTGAGAATA
TCTCTCCCTATGGCAATCTGGAGCTTAAAGGGGAAACTTATTCTCAAAATGAGAGTATGAGGAC
AGATATTGTTAGTACTGAGTAACTGCTAGTGTGCGGGTGGTTTCAATGTTCTCATGTTAAAGGTTAGAAGG
TTCTCATTTGTCATGGGATGATGTTGAGATTTTTTTTTTAAAGAGATCTTCAAGGAAACACAGTTCAGAGAG
ATTTCATCGGGTGCACTCTCTGCTCTGGTGTGACAAGTATCTGGCTGCTGAGAAAGAGTGCCTGCC
ACACCGGGAGACCTTCTCTCACCTCATGAGTATGTTGAGTCTTCTGTCATTAACTGGTAAAGGAGGGCTGG
AGAACAGTAAATTTTGAGACAAATGGTACAATAGAAGGCTTCTGGTAAAGGAGGGCTGG
AGGGGGAAAATAATCATTAAGGCTTGGAGTAAACGGCAAGAATATGGCTGAGTCCATTAAATGGTCAATT
TCCCTTATGGTCATATAACTGCAAGCTGAGATGAAAGGGGAAAATAATGAAAATTTTACTTTGAGTCCAA
TGATATACATGCACTAAACTGATGGGAAAGGTTATCCTAAAGTACTGTTATACATCTGTTTATTATTTAATGTTT
CTAAAAAATTTGTTGAGTGGTTTCCCAATGGCTAAATAAAAACAAATTATTGTAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVQCQ
RCKHGE C1GPNKCKC HPGYAGKTCNQDLNECGLKPRPC K HRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDGRITCVDVDECATGRASCPFRQC
VNTFGS YICKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKC KEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNNWIPDVGSTWPPKTPYI PPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTT PERPTTGLTTIAPA AASTPPGGITVDN
RVQTDPQKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRD PAGGQYLTVAAKAPGG
KAARLVLPLGRLMHSGDLC SFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQ TQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTCTAGATTGTGA
AATGTGGCTCAAGGCTTCAACATTCTTCTTCTTGCACAGGTGCTTGTCTGGGGCTGA
AGGTGACAGTGGCCATCACACACTGTCATGGCGTCAGGGCTCAGGGCTCTACCTACCGCTC
CACTATGCCCTACACTTCAGCATCAGACATCCAGATCATATGGCTATTGCTGAGAGACCCCA
ACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTCTGACTTGGAAATACC
AACACAATCTCACCAGTGGCCACCAATGCATCTCCTGTTATCAACCCACTGCAGTTCCCT
GTAGAAGGCAATTATCATCTGTGAAGGTCAACATTAGGGAAATGGAAACTCTATCTGGCCAGTCA
GAAGATAACAAGTCACTGGTGTATGATCTCTGCACAAAGCCAGTGTGCAAGATTCTATCCTCCCT
CTGGGGCTGTGGAGTTATGGGGAAACATGACCCCTGACATGCCATGTGGAAGGGGCACTCGG
CTAGCTTACAATGGCTAAAAATGGGAGACCTGTCACACAGCTTCCACTACTCTTTTC
TCCCCAAAACAAATACCTCTATATTGCTCCAGTAACCAAGGAAGACATGGGAAATTACAGCT
GCCTGGTAGGAACCTGTCAGTAATGGAAAGTGTATATTATGCCCATCATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGAAAGTGTAACTGT
TGACCTTGGAGAGGCCATCTTGTGATTTCTGTGATTCTCATCCCCAACACCTACT
CTGGGATTAGGGAGGACTGACAATACTACATATCATTAAGTCATGGGCTCTGTTAGGTT
GCATCTGAGAAAGTAGCCAGAAGACAATGGACTATGTGTGCTGTGTTACAACACATAAC
CGGGCAGGCAAGTGAACACTATTCAACAGTTATCATCTCCCTGAGGACTGGAGAAGCTTG
CACAGAAAGGAAATCATGTCCACCTTACAGGAACTTACATATTCTTGTGATT
ATATCCATGTGCTTCTCTTCTATGGAAAAAAATCATACCCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAACATCAGGAAAGCTAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCCGAATATATGAATTCTGTGTTTCCAGATGTTCTGTGTTTCCAGG
ATTCCAACAGGCTGTCTTCCACCTCTGATTGTGTTCTGGGAAAGATTGCAAGTACAGT
GTATGAAGTTTACGCACATCCCTGCCAGCAGAACATCAGAGTGAACATTCTGTGG
GCTAAACAGTACATTGAGTGAATTCTGAAGAACATTAAAGGAAAAACAGTGGAAAAGT
ATATAATCTGGAAATCAGTGAAGAACACAGGCCAACCTTCTTACATTATCTTCTTACA
TGCAAGAATAGGGCTATTATGCAAAATTGAACTGCAGGTTTCTCAGCATATAACACATGTCT
GTGCAACAGAAAAACATGTTGGGAAATTCTCTCAGTGGAGACTCGCTCTCATGTCAGCG
GGAGAACGAAAGTGACAGGGTTCTCTATAAGTTGTATGAAATATCTACAAACCTCA
ATTAGTTCTACTCTACATTCACTATCATCACACACTGAGACTTCTGTGTCACCTACAAAA
TGTGGAAACTTCTACATTGTTGAGACTTCTCAGCAGACTTGTGTTTATTAAATTCTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTATTTCTACAAATTCTACATTCTGTGTTATTGTCAA
CAAAGTAATTAAGGAGTGGTGTCAACAAAACAAACTATGCCCTCTCTTTTCTTCAATCACC
AGTAGTATTGAGAAGACTGTGAAACCTAAGGAAATGACTTAAAGTCTTATTTTCA
TTTTTCTAAGGAAAATGATGATCCTAAATAATTATCTGTGTTTGTGTTTATTAAAGTCTTATTTTCA

FIGURE 112

MWLVKFTTFLSFATGACSGLKTVPSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNVKSVVPDLEYQHKFTMMPNAPASLLINPLQFPDEGNYIVKVNIQGNGTSLASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNTLTCHVEGGTRLAYQWLKNGRPVHTSSTSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPyGLQVNSDKGLKVGEVFTV
DLGEA1LFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHEFTVIITSVGLKLAQKGKSLSPASITG1SLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAGCGGCCGAAATGGGCCCTCGGGAGTCTTGCACTCCCTGGCAGTCCTGGTGTGTT
GCTTGGGGTGTCTCCCTGGACCGCACGGGGCGGAGCAAGCTCGCGTCATCACGGACGAGA
ACTGGAGAGAACCTGCTGGAAAGGAGACTGGATGATAAGATTATGCCCGTGGTGCCTGCT
TGTCAAAATCTCAACCGGAATGGAAAGTTTGCTGAATGGGAGAAAGATCTGAGGTTAA
TATTGCAAAGTAGATCTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCTACTATTATCATTGAAAGATGGTGAATTAGGGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAACTGATAAAAGACTGGAAAGACTATTGAGGCCGTTTCATCATG
GTTGGTCCAGGTTCTGATGAGTAGTGTCAAGCACTTTCACTATCTATGTGGA
TCAGGACGTGCACTAACTTTATGAAAGACCTGGATGCCAGTGGGGAGTCATAACT
GTTTGTGCTTGAACCTGTTCCGGACTTATTAGGACTCTGTATGATAATTGTC
AGATTGCCCTTGCTCTCAAAAAGCGCAGACCCACAGCCATACCCATACCCCTCAAAAAT
TATTATCAGAACTGACACAACTTGTGAAAGAGTGGAGGAGGAACAGAGGCGATGAAGAA
GATGTTTCAGAAGAAGCTGAAAGTAAGAAGGAACAAACAAAGACTTCCACAGAATGC
CATAAAGCAACGCTCTGGGCATCATTGCCACAGATAATCC**TAGTTAAATT**TATAG
TTATCTTAATATTATGATAAAAACAGAAGATTGATCATTTGTTGGTTGAAGTG
AACTGTGACTTTTGATATTGCAAGGGTCAAGTCTAGATTGATTAATTGAGAGTCTA
CATTGAGAACATAAAAAGCACTAGTATCACAGTTGAAATATGATTTAACAGCAGTGTG
GTTAAATAGTCTCTAATTGAAAAATCTGTCAGCAAGCAATAAGATTATGATATTG
TTAATAAAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGCAATTAT
TGAGGTATTAAGAAGATTATTGAGAAAATTACATTCTCATTTGATAATTGTTCTG
TTCACTGTGAAAAAAAGAAGATATTCCCATAAATGGGAAGTGGCCATTGCTCAAG
AAATGTGATTTCAGTGACAATTCTGGTTAGAGGTATATTCCAAAATTCTGT
ATTTTAGGTATGCAACTAAAAAACACTTCAATTAAATTACAGTTTCTACACA
TGGAATACAGGATATGCTACTGATTAGGAGTTTTAAGTTCATGGTATTCTTGATT
CAACAAAGTTGATTTCTCTGTATTTCCTACTATGGGTACATTTTTATT
CAAATTGGATGATAATTCTGGAAACATTTTTATGTTTGTAAACAGTATTTTGGT
GTTTCAAATGAGTTTACTGAGAGATCCATTGACAATTGTGAAATTAA
TTGGCACTTTTCAGATTTACATCATTCTGCTGAACCTCAACTTGAATTGTTTT
TTTCTTTTGATGTTGAGGTGAACTTCTGATTTTGCTGATGTGAAAAAGCCTGGTA
TTTACATTGGAAAGCTTCAAGGCTTAAATAAAAGTTGCAATTCTACTCAGGAAAAG
CATCTTCTGTATACTGCTTAAATGTTGTCCTCATACAGAAAGTTCTAATTGAT
TTACAGTCTGTAATGCTGTGTTAAAATAACATTATTATTTTAAAGACAA
ACTTCATATTCTCTGTTCTTCTGACTGGTAATATTGTGTTGGGATTTCACAGGAAAA
GTCAGTAGGATGGAACATTTAGTGTATTCTACTCCTAAAGAGCTAGAATACATAGTTT
CACCTTAAAGAAGGGGGAAATCATAAATACAATGAATCAACTGACCATTCAGTAGAC
AATTCTGTAAATGTCCTTCTAGGCTCTGTTGCTGTGTAATCATTAGATTACAG
TATCGTAATATAACAGTTTCTTAAAGCCCTCTCTTAAAGATTTAAATATTGTACCTT
AAAGAGTTGGATGTTGTAACCTGTGATGCCCTAGAAAATATCCTAACGACACAAATTAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDW MIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCP SKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGP SLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCAGGTGTCAGCTGCGGAGACCGTGTATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGAAGCAGTGTCAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
AAGGTCTGCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGCTGC
ATTGCTGATGCCCTGTTGGTCTGTGAGCTGTGTCAGGCGGAATTCTTACACCTCTATTG
GGCACATGACTGACCTGATTATGAGAGAAAGAGCTGGTCAGTCTGTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCAAGATTAAGAGCTGGGCAACAAAATGGAAGGCCTTGAC
TAGCAAGTCAGCTGTGAGGGCTACCTGGCTCACCTGTAAATGCCAACAACTGG
TGAAGCGGCTAAACACAGACTGGCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGGGCAGTTCTCCCACTGTAGAGGACAGGAGATAGG
AGCTGCCAACGGCTGTAGAGACTTCAAGGACACATAAGGGCTGGACCCAGGCACATTCTCA
GAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGATGACTGCTTGGGATG
GGCGCTCGGCCCTAACATGAGGGACTATTATCATCGCTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTGTGATGCCGGGGAGGGAGGCCAACAAACAGTACAGGTGCTGAGACTACCTCA
GCTATGCTGCTTCAGTTGGGTGATCTGACCGTGTGCTGGAGCTCACCGCCGCTGCTC
TCCCTTGACCCAAAGCCAGCACAGAGCTGGAGGAATCTGGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAACAGCA
TCTATGAGAGGGCTGTGGACTACCTGCTGAGAGGGATGTTACGAGAGCCTCTGCTGG
GAGGGGTGCTCAAACGTACACCCCGTAGACAGAAAGAGGCTTCTGTTAGGTACCACTGGCAA
CAGGGGCCCCACAGCTGCTGCTGGCCCTTCAAAGAGGAGGAGCAGGTGGGACGCCGACA
TCGGTCAAGGACTACTAGATGTCTGTGAGGGAAATCGAGAGGATCAAGGAGATCGCAAA
CCTAAACTTGACGAGCCACCGTGTGATCCAAAGCAGGAGTCTCTACTGTGCGCAGCTA
CCGGGTTTCCAAAAGCTCTGGCTAGAGGAAGATGATGACCCCTGTTGGCCCGAGTAAATC
GTCGGATGCGACATCATCACAGGGTAAACAGTAAAGACTTGCGAGAAATTGTTACAGGTTGCAAAAT
TATGGAGTGGGAGGACAGTATGAAACCGACTTCGACTTCTCTAGGGCACCTTTGACAGCGG
CCTAAACAGAGGGAAATAGGTAGCGACGTTCTAAACTACATGAGTGTAGAAGCTG
GTGGTGCCACCGCTTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTG
TTCTGGTACAACCTCTGGAGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCCTGCC
TGTGTTGTGGCTGCAAGTGGGCTCCAAATAAGTGTGTTCTAGAACGAGGACAGGAGTCT
TGAGACCTTGTGGATCAACAGAAGTGTGACCTGACATCCTTTCTGCTCTCCCTTCTGGTC
CTTCAGCCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTTATCAGGCT
GATTTTGAGGAAATGAATGTTGTGAGGAGCAGAGGGAGACCATACTAGGGGACTCTGT
GTGACTGAAAGTCCCAGCCCTTCATTGAGCTGTGCCATCCCTGGCCCAAGGCTAGGATCA
AAAGTGGCTGAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCCTTGTACCTCAGGGTT
TTAGGTGTGAGATGTTCTAGTAACCAAGTCTGATACCTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACAAAAAATGCCCCAACAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVVEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSQLVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLQKLDAGEEATTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLEEEEREKTLTNQTEAELATPEGIYERPVVDYLPERDVTYESLCRGEGVKLTPRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNRRMHOITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGLDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

FIGURE 118

MRLSSLLALLRPALPLILGLISLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNPKVVKLTRYIQTTELGSRERLLVAVLTSRATLSTLAVANRTV
AHHFPRLLYFTGQRGARAPAGMQVVSQHDERPAWLMSETRLHLHTHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLLDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGPKCPLQGASRADVGALETALEQCLNRRYQPLRFQKQRLLNGYR
RFPDPARGMSEYTLDDLLECVTQRGHRALARRVSLLRPLSRVEILPMPYVTEATRVQLVPLLL
VAEAAAAPAFLEAFANAVLEPREHALLTLLVYGPREGGRGAPDPFLGVKA AAAAEELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFLTTVWTRPGPEVLRNCRMNAISGWQAFFP
VHFQEFNPALSPQRSPGPPGAGPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEEEALEGLEVMDVFLRFSGHLHFLRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAACCGTGC CGGCTGCGCTTCCGTCCCCAAGCC
GTTCTAGACGCCGGGGAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAAGAAGATATCTTGA
GAGGATGAGCGCATGGAGCTAGTAAGAGCTTGCAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGAGTAAAGGAGACTTGGACCAACACTGTGACAAGCAG
AGTTCTTCAGTCTGAAAATGTTAAAGTGTGAGTCATTAAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAAATACGCTTGTATAAGTATAGAGACCAATACAACTG
GTTCCTTGACGCCCACTACGTTGCTCATGAAAACCTAAAGTATTGGTTAA
AAAAGGATCCATCACGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGCTTAAGTGTAGAATCAATGAAAAGACTAACAGCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAAACCAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTATCACCC
CAACAGGTAGTAGAAGGCTTGTCTCAGATATGGCTTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTATGGGTATACCGCCTTAGGGCATTTGGCATATTTCAT
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTTGTCAATTGGTAGTAGTAACATATCCAA
TACAGCTGTATGTTCTTTCTAACTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAACACATGAACATTGTAATG
TGGTGGAAAGAAGTGTAAAGATAATAATTGGCAAAACTATTAAATAATATTAT
GTGATAAAATTCTAAATTATGAAACATTAGAAATCTGGGGCACATATTGGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCTAAAGATATGCAAATGATATCTCTAGTTGTAATT
TGTGATTAAAGTAAAACCTTGTGTTCCCTTACTCTAAACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCTTCTCAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLAAVAKETWTKHCDKAEFFSSENVKVFESINMDTNMDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

FIGURE 122

MNSSKSSETQCTERGCFSSQMLWTVAGIPIFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTTELSCNYGGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDTPLTKSLSFWDVGEPENNIATLEDATMRDSS
NPRQNWNNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCGCGCTGCCGCTGGCCCTCTAGCAACCCCTGACATGGCGCTGAGGCCGACCGCGAC
TCCGGCTCTCGCTCGCTCGCTGACTCTCTCTCTGCTCTGCTTTCAGGGCTGCTGATAGGGCTGTAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGATGTGAAACTGTCTTGACATCATTAAGGATTCC
AGACAACTGACCCAGGGCTGAGGAAAGAAATTCAAGATGAAACAAACACATATGTTTTTGACACAAAAA
TTTGGGAGACTTGGCGGGTCTGCAAAATACTGGGAGACATCCCTGAGAATCTGAAATGTGACACGGAG
ACTCAGCCCTTATCGCTGAGGCTGGTCTGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGGACCCCTGCTGAGGTGCGGAGGGCTGACAGCTGGTATCGCAATGATGTA
ACTGCGAGGAGTGGAGGGCCACCCCGCCCTACTACAGCTGGTATCGCAATGATGTA
ACTGCGAGGAGTGGAGGGCCACCCCGCCCTACTACAGCTGGTATCGCAATGATGTA
CCAGAACCATACTCCAGAATTTCGCACTTCTTCTTCACTTAAACTCTGAAACAGGCACTTTGGTGTCTGACTGCTG
TTCACAGGACACTCTGGGAGTACTACTGCTATGCTTCAACTGACCCAGGCTGAGCAGGTGAGGAGCAGG
AGATGGAAGTCTAGCTGACCAATTCGCGGAATTATTGGGGGGTCTGGTTGCTGACTGGGCTCTGA
TCACTGGGGCATCTGCTGTCATACAGCTGGTCTACTCATCAACAAACAGGATGGAGAAACTTAAAGA
ACCCAGGAAACAGATGGATTAACATACATCCGCACTGACGGAGGAGGGACTTCAGACACAAAGTCACTGTTT
TGATCTGAGACCCCGGGTGTGGCTGAGGCGACAGACGGCACTGGTACACATCTCTGCTGAGAAACTCCGTCAA
GGCAGGAGAGCTGAGCTGACTCGCGACAGCTGACACTTCACTTCAAGAAGTGGACCCGGTAAATAACACCAA
CTACTCTTCTTCAACTAAAGCAGTGGGATTAAGAAGAATTCTCTGCAAGATGGACCCGGTAAATAACACCAA
GGAGGCGAAACTGGGGTGTGGTCACTGAGTTGGGTTCTAATCTGTTTCTGCTGATTCGGCATGAGTATTAG
GTGATCTTAAAGAGTTGCTCACGTAACGGCCCTGCTGGCCCTGTGAGGAGCAGTGTCACTGGTGTG
CAGCAGCCAGGACGACCCAGTGGATGGAGTGGAGGAGGGTGTGGAGCAGCACCCAGGGCATCCGGGGAAACCA
GAAAAGGGTTCTTCAACAGCGCTTCACTTCAGGCGGACAGACACCCAGGTTCTTCTTAAAGGCTCTG
TGATGAGTGTGAGCTGTCATTGAGGAGCTTGGTGAATGAGCCTTTGGTAACTTGGTCTGAGGAACTTGGAAA
GTAIAATTGGTTGCTGGAGGAGTCTGCTGAGGAACTCTGCTGAGGAACTCTGCTGAGGAACTTGGAAA
ACCTTCGTTAGGCTAAGTGTGAAATGGTACTGAAATATGCTTCTATGGTCTTGTGTTTAAATTAAATT
TACATCATTAATTGGTCAAGGATGTTGGTAAATTGAGAAGAAATTCTTAAACTGAGAAGTTCAACT
CATACATGTTAAATAACCTTATTTTAAAGGACTTCAACTTAAGGATGTTCAACT
TGGAAAATCTAATAAAGGATTTTACCAAGGAACTCTCTCTGAGGAACTTCTGAGGAACTTCTTCT
CACACAAAGTCTTACAGGAACTTCTTCAACAGGAACTCATCTGCTACACATCAGACCATAGTGTGTTAGGAAACCTT
TAAAATTCAGTAAAGCAATGTTGAATCAGTGGCATCTTCTCTTAAAGAAACCTCTCAGGTTAGCTGAACT
GCCCTCTTCTGGAGTACTAGGGACACTGTCACCGGGAGGCCACCCAGGGCCCTAGCTGCTGCTGCTGAGGAGGGCC
CCAGTCACTGGGGTCTGGGGTCTGGGGAGGCCACCCAGGGCCCTAGCTGCTGCTGCTGAGGAGGGCC
GCCACTTCTGGGGGACATTAGCAACATCAGAACGGCTGCTGCTTCCAGGCTGACTGACCTTACTGACCTGCT
TCTCAGGGGCACTGGGGCACTGGGGTCTTCCAGTGGCTGCTGCTGCTGCTGAGGAGGGCC
TTTGGGTTATGGATGGCTCAAAAGATAAGGGCCCTCAAGTCTTCTTAAAGTTGTTTAAATTGGT
AAGATTCTAAGGCAAAAGCAATTGGAAATCTAGCTGCTGAGTAACTAAACATTTTAAAGAAATTGGAT
CCCACTGTTCTCTTGCACAGAGAAAGCACCCAGGCCACAGGCTCTGCGCATTTCAACAAACCATGAT
GGAGTGGGGCACTGGCAACCTTGGTAAAGAAGCTGAGGGAGCAGCAGGTTAGCTGAAAGGGCTGGGGGGAGGAAAG
TGAACCCCTGAATAAAAGCAGTTTCTAATTTCAGTGGGGAGACACTGCTCCT
TGTGGGGGACATTAGCAACATCAGAACGGCTGCTGCTTCCAGGAGGAGTGTCTCAGGCTTACATGCCCT
GCCCTGTTGGAGACTGGAGCTGAGTGTGTTAAAGCAAGGAGCTGCTGAGGAGGAGCACTTCACTGTGCTGCTG
GAATGGCTCACTACTCACCTGCTTCACTGCTGGGTTTTTAACTTGTGACAGCTTCTT
AATTGCACTACATGAGACTGTTGACTTTTTAGTTGAGAAACACTTGGGGAGGCCGCTGGAGGGCA
GGAAATCTCCAGAGTGGCTCAGGCTCTGGTCTGCTGCACTGGCATCTGGATGCTTACATGCAAGTTC
CCTCCATCATGGCACCTTGGTAAAGAAGCTGAGGGAGTGGCTCCACCTCAAGGCTTGGGATTCACTGGCTCAGGCTT
TCTTGGGTTGTCATACTGATAGGGTACCTTATGCCCCCTCTCTTAAACCTTACACTAGTGTCCA
TGGGAAACCGGTCTGAAAAAGTAGAGGAGAAGTGAAGTAGAGTGTGAGTCTGCTCTATAACTGAGACTAGA
CGGAAAAGGAATACTGCTGTTGAGGAGAAGTGAAGTAGAGTGTGACTCAAGACTGAGGAGGCCATACAGGCTGATTCT
GCCCTTGGATGAGTTGCTGTCACAGATGCTACAGACTTGTACTAAACACCGTAATTGGCATTGTTAAC
CTCATTTAAAAAGCTTCAAAAAACCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPPLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIAASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSFVI
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Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267